

TABLE 1

Bacteriophage 44AHJD, complete genome sequence.

1 tccattttctt tactaaactt aaaaatgctg tgcaacaact taaccaactt atctaacct
 61 ttacatatc atcaaataca aaatttatgt atctattgac ttttattcaa aattatgatt
 121 tcaacatata ataaaattaa ttactttatt taaatattct atgatataat tagttataaa
 181 atatttggag gtgtataaat gacagaattt gatgaaatcg taaaaccaga cgacaaagaa
 241 gaaacttcag aatcaactga agaaaattta gaatcaactg aagaaacttc agaatcaact
 301 gaagaatcaa ctgaagaatc aactgaagaa tcaactgaag ataaaacagt agaaacaatc
 361 gaagaagaaa atgaaaacaa attagaacct actacaacag atgaagatag ttcgaaatct
 421 gaccctgttg tattagaaca acgtattgct tcattagaac aacaagtgac tactttttta
 481 tcttcacaaa tgcaacaacc acaacaagta caacaaacac aatcagatgt aacagaatca
 541 aacaaagaag ataacgacta ttcagatgaa gaactagttg ataagttaga tttagattag
 601 gaggaattta aacatgtatg agggaaacaa catgcgttct atgatgggta catcatatga
 661 agattcaaga ttaaataaac gaacagaatt aaatgaaaac atgtcaattg atacaaataa
 721 aagtgaagat agttatggtg tacaatttca ttcactttca aaacaatcat ttacaggtga
 781 cgttgaggag gaataataaa ttatggcaca acaatctaca aaaaatgaaa ctgcactttt
 841 agtagcaaag tcagctaaat cagcgttaca agattttaat catgattatt caaaatcttg
 901 gacatttggc gacaaatggg ataattcaaa tacaatgttc gaaacatttg taaataaata
 961 tttattccct aagattaatg agactttatt aatcgatatt gcattaggta atcgttttta
 1021 ttggttagct aaagagcaag attttattgg acaatatagt gaagaatacg tgattatgga
 1081 cacagtacca attaatcatg acttatctaa aaatgaggaa ttaatgttga aacgtaatta
 1141 tccacgtatg gcaactaagt tatatggtta cggaattgtg aagaaacaaa aattcacatt
 1201 aaacaacaat gatacacgtt tcaatttcca aacattagca gacgcaacta attacgcttt
 1261 aggtgtatag aaaaagaaaa tttctgatat taatgtatta gaagaaaaag aaatgcgtgc
 1321 aatgttagtt gattactcat tgaatcaatt atccgaaaca aatgtacgta aagcaacatc
 1381 aaaagaagat ttagcaagca aagtttttga agcaatccta aacttacaaa acaacagtgc
 1441 taaatataat gaagtacatc gtgcatcagg tgggtgcaatt ggacaatata caactgtatc
 1501 aaaattaaaa gatattgtga ttttaacaac agattcatta aaatcttata ttttagatac
 1561 taagattgca aacacattcc agattgcagg cattgatttc acagatcacg ttattagttt
 1621 tgacgactta ggtggcgtgt ttaaagtaac aaaagaatct aagttacaaa accaagattc
 1681 aattgacttt ttacgtgcgt atggagatta tcaatcaca ttaggagata caattccagt
 1741 tgggtgctgta tttacttatg atgtatctaa acttaaagag tttactggca acgttgaaga
 1801 aattaaacca aaatcagatt tatatgcgtt tattttggat attaatcaa ttaaataata
 1861 acgttacaca aaaggtatgt taaaaccacc attccataac cctgaatttg atgaagttac
 1921 aactggatt cattactatt catttaaagc cattagtcca ttctttaata aaattttaat
 1981 tactgaccaa gatgtaaatc caaaaccaga ggaagaatta caagaataaa aggagcgtaa
 2041 aatatgaaca acgataaaag aggtttaaac gttgagttat caaaggaaat cagcaaaaga
 2101 gttgttgaa acgcgaacag atttaaacgt cttatgttta atcgttattt ggaattttta
 2161 ccgctactaa tcaactatac caatcgtgat acggttggtg tagattttat tcagttagaa
 2221 tcagctttta gacaaaacat taatgtagtt gttggtgaag ctagaaataa gcaaattatg
 2281 attcttgggt atgtaaataa cacttacttt aatcaagcac caaatttttc atcaaacttt
 2341 aatttccaat ttcaaaaacg attaactaaa gaagatatat attttattgt acctgactat
 2401 ttaataacct atgattgtct acaaattcat aagctatatg ataactgtat gagtggtaac
 2461 tttgttgtca tgcaaaataa accaattcaa tataatagtg atatagaaat tatagaacat
 2521 tatactgatg aattagcaga agttgcttta tctcgctttt cttaaatcat gcaagcaaaa
 2581 ttttagcaaga tatttaaatc agaaattaat gacgagtc aaatcaact tgtgtccgaa
 2641 atatataacg gtgcaccatt tgttaaaatg tcacctatgt ttaatgcaga tgacgatatc
 2701 attgatttaa caagtaatag cgtaatccca gcattaactg aaatgaaacg ggaatatcaa
 2761 aacaaaatta gtgaattaag taactattta ggcattaatt cattagccgt tgataaagaa
 2821 agcgggtgtt cagacgaaga ggcaaaaagt aatcgtggat ttaccacatc aaacagtaat
 2881 atctatttaa aaggctcgtg accaattacg tttttatcaa agcgttatgg tttagatatt
 2941 aaacggtatt acgatgatga aacaacgtct aaaatatcaa tggtagacac acttttttaa
 3001 gatgaaagca gtgatataaa tggctagata cacaatgact ttatacgatt tcattaaatc

GenBank: 268226

TABLE 1

3061	agaattgatt	aaaaaagggt	tcaatgaatt	tgtaaatgat	aataaattaa	cgttttatga
3121	tgatgaat	caattcatgc	aaaaaatgct	gaagttcgac	aaagacgttt	tagctatcgt
3181	taatgaaaa	gtatttaaa	gtttttcatt	gaaagatgaa	ttatcagatt	tactttttaa
3241	aaaatcatt	acgattcatt	ttttagatag	agaaatcaac	agacaaacag	ttgaagcatt
3301	tggcatgcaa	gtgattactg	tatgtattac	acatgaggat	tatttaaatg	tggttttattc
3361	atcaagtga	gttgaaaaat	acttacaatc	acaaggcttc	acagaacaca	atgaagatac
3421	aacaagtaac	actgatgaaa	catcgaatca	aaatgctaca	tcttttagaca	attcaactgg
3481	catgactgca	aacagaaacg	cttatgtgtc	attaccacaa	agtgagggtta	acattgatgt
3541	tgataataca	acgttacgat	tcgctgataa	taatacgatt	gataacggta	aaactgtgaa
3601	taaatcgagt	aacgaaagta	atcaaaacgc	aaaacgtaat	caaaatcaaa	aaggtaatgc
3661	aaaaggta	caattcacta	agcagtattt	aattgataat	attgataaag	cgtacgattt
3721	aagaaagaaa	attttaaatg	aatttgataa	aaaatgtttt	ttacaaattt	ggtagagggtg
3781	gttaataaat	ggcatataat	gaaaacgatt	ttaaatat	tgatgacatt	cgtccatttt
3841	tagacgaaat	ttataaaaacg	agagaacggt	atacaccggt	ttacgatgat	agagcagatt
3901	ataatactaa	ttcaaaatca	tattatgatt	atatttcaag	attatcaaaa	ctaattgaag
3961	tattagcacg	tcgtatttgg	gactatgaca	atgaattaaa	aaaacgtttc	aaaaattggg
4021	acgacttaat	gaaagcattt	ccagagcaag	cgaaagactt	atthagagggt	tgggttaa
4081	acggtacgat	tgacagtatt	attcatgacg	agtttaaaaa	atatagcgca	ggattaacat
4141	cggcatttgc	tttattttaa	gttactgaaa	tgaacaaat	gaatgacttt	aaatcagaag
4201	ttaaagactt	aattaaagat	attgaccggt	tcgttaatgg	gtttgaatta	aatgagcttg
4261	aaccaaagtt	tgtgatgggc	tttggtggta	ttcgcaacgc	agttaacca	tctattaata
4321	ttgataaaga	aacaaatcac	atgtactcta	cacaatccga	ttctcaaaaa	cctgaagggt
4381	tttgataaaa	taaattaaca	cctagtgggtg	acttaatttc	aagcatgcgt	attgtacagg
4441	gtggtcatgg	tacaacaatc	ggattagaac	gtcaatccaa	tgggtgaaatg	aaaatctgggt
4501	tacatcacga	tgggtgttgc	aaactgttac	aagtcgcata	taaagataat	tatgtattag
4561	atttagaaga	ggctaaagggt	ttaacagatt	atacaccaca	gtcactttta	aacaaacaca
4621	catttacacc	gttaattgat	gaagcaaatg	acaaactcat	tttaagattc	gggtgacggaa
4681	caatacaggt	tcgttcaaga	gcagacgtaa	aaaatcacat	tgataatgta	gaaaaagaaa
4741	tgacaattga	taattcagaa	aacaatgata	atcggttggat	gcaaggcatt	gctgttgatg
4801	gtgatgattt	atactgggtta	agtggtaaca	gttcagttaa	ttcacatggt	caaactgggtta
4861	aatattcatt	aacaacaggt	caaaagattt	atgattatcc	atttaagtta	tcatatcaag
4921	acggtattaa	tttccacgt	gataacttta	aagagcctga	gggtatttgc	atttatacaa
4981	atccaaaaac	aaaacgtaaa	tcgttattac	ttgctatgac	aaacggcggt	gggtggaaaac
5041	gtttccataa	tttatatggt	ttcttccaac	ttgggtgagta	tgaacacttt	gaagcattac
5101	gcgcaagagg	ttcacaaaac	tataaattaa	caaaagacga	cggctgtgca	ttatctattc
5161	cagaccatat	cgacgattta	aatgacttaa	cgcaagctgg	tttttattat	attgacgggg
5221	gtactgcaga	aaaacttaag	aatatgccaa	tgaatggtag	caagcgtata	attgacgctg
5281	gttggttcat	taatgtat	cctacaacac	aaacattagg	tacggttcaa	gaattaacac
5341	gtttctcaac	aggctgtaaa	atgggttaaaa	tgggtgcgtgg	tatgacttta	gacgtattta
5401	cgttaaaatg	ggattatgga	ttatggacaa	caatcaaaac	tgacgcacca	tatcaagaat
5461	atttgggaagc	aagtcaatac	aataactgga	ttgcttatgt	aacaacagct	gggtgagtatt
5521	acattacagg	taaccaaatg	gaattattta	gagacgcgcc	agaagaaatt	aaaaaagtgg
5581	gtgcatgggt	acgtgtgtca	agtggtaacg	cagtcgggtga	agtaagacaa	acattagagg
5641	ctaataatc	ggaatataaa	gaattcttca	gtaatgttaa	tgcggaaaca	aaacatcgtg
5701	aatatgggtg	ggtagcaaaa	catcaaaaat	aggagtgata	taaatgaaat	cacaacaaca
5761	agcaaaagaa	tggatatata	agcatgaggg	ggcagggtgtt	gactttgatg	gtgcatatgg
5821	atttcaatgt	atggacttat	cagttgctta	tgtgtattac	attactgacg	gtaaagttcg
5881	catgtgggggt	aatgctaaag	acgcgataaa	taatgacttt	aaagggttag	cgacgggtgta
5941	taaaaataca	ccgagcttta	aacctcaatt	aggggacggt	gctgtatata	caaattggaca
6001	atatggacat	attcaatgtg	tgttaagtgg	aaatcttgat	tattatacat	gcttagaaca
6061	aaactgggtta	ggcggcggtt	ttgacgggtg	ggaaaaagca	accattagaa	cacattatta
6121	tgacgggtgta	actcacttta	ttagacctaa	attttcagggt	agtaatagca	aagcattaga
6181	aacatcaaaa	gtaaatacat	ttggaaaatg	gaaacgaaac	caatacggca	catattatag

TABLE 1

6241	aaatgaaaat	ggtacattta	catgtggttt	tttaccaata	tttgcaogtg	tcggtagtcc
6301	aaaattatca	gaacctaatg	gctattgggt	ccaaccaaac	ggttatacac	catataacga
6361	agtttggtta	tcagatgggt	acgtatggat	tggttataac	tggaaggca	caggttatta
6421	tttaccagtg	cgccaatgga	atggaaaaac	aggtaatagt	tacagtgttg	gtattccttg
6481	gggggtgttc	tcataatggg	tatttttagcc	tttttctttg	aatttagttg	gaaaagatac
6541	aaataagagg	tgtaaacaat	ggctgataga	atcgtaagaa	gtttaagaca	agttgaaaca
6601	attgaacggt	tattggagga	aaaaaatgag	aaagttaacg	aattttaagt	ttttctataa
6661	cacaccgttt	acagactatc	aaaacacgat	tcattttaat	agtaataaag	aacgtgatga
6721	ttatttttta	aatgggtcgt	attttaaatc	gttagactat	tcaaaacaac	cgtataattt
6781	tatacgtgat	agaatggaaa	tcaatgttga	tatgcagtgg	catgacgcac	aagggtattaa
6841	ctacatgacg	tttttatcag	attttgagga	tagaagatat	tacgcttttg	taaaccaa
6901	cgaatacgtg	aatgacgttg	tggttaaaat	atattttgtc	attgatacca	ttatgacgta
6961	tacacaaggg	aatgtattag	agcaactctc	aaacgtcaat	attgaacgtc	aacattttatc
7021	aaaacgcacg	tataactata	tgttaccaat	gttacgtaat	aatgatgatg	tggtaaaagt
7081	atcaaatata	aactatgttt	ataaccaa	gcaacaatat	ttggaaaatt	tagtattatt
7141	ccagtcaagc	gctgatttat	caaagaaatt	tggtactaaa	aaagagccaa	acttagatac
7201	gtcaaaaggt	acgattttatg	acaatatcac	atcaccagtc	aacttatacg	ttatggaata
7261	tggtgacttt	attaacttta	tggtataaaat	gagtgcctat	ccatggatta	cgcaaaactt
7321	tcaaaaggtt	caaagtgttac	ctaaagactt	tattaatata	aaagacttag	aggacgttaa
7381	aaccagtgaa	aaaattacag	gattaaaaac	attaaaacag	gggtggtaaat	caaaagaatg
7441	gagtctaaaa	gatttatcat	taagtttctc	aaatcttcaa	gagatgatgt	tatctaaaaa
7501	agatgaattt	aaacatatga	tacgtaatga	gtatatgaca	attgaatttt	atgactggaa
7561	tggaataacg	atgttactcg	acgctggtaa	gatttcacaa	aaaactgggtg	ttaagttacg
7621	tacaaaatca	attattgggt	atcataatga	agttcgagta	tatccagtag	attataacag
7681	tgctgaaaac	gacagaccaa	tactcgctaa	aaataaagaa	atattgattg	atacgggttc
7741	attcttaaat	acaaatataa	catttaatag	ttttgcacaa	gtaccaatat	taatcaataa
7801	tggtatctta	ggacaatcac	aacaagccaa	ccgacaaaaa	aatgcagaaa	gtcaattaat
7861	tacaaatcgt	attgataatg	tattaaatgg	tagcgacccg	aaatcacgct	tttatgacgc
7921	tgtgagtgtg	gcaagtaatt	taagtccaac	tgctttat	ggtaagttta	atgaagaata
7981	taatttctac	aaacaacaac	aagctgaata	taaagattta	gccttacaac	caccttctgt
8041	aactgaatca	gaaatgggca	acgcattcca	aattgcgaat	agcattaacg	gtttaacgat
8101	gaaaattagt	gtaccgtcac	ctaaagaaat	tacattttta	caaaaatatt	atatgttggt
8161	tggttttgaa	gtgaatgact	ataattcatt	tattgaacca	attaacagta	tgactgtttg
8221	caattattta	aaatgtacag	gtacgtatac	tatacgtgac	atcgacccca	tggtaatgga
8281	acaattaaaa	gcaatttttag	aatctgggtg	aagatttttg	cataatgacg	gttcagggtaa
8341	tccaatgtta	caaaatccat	taaataacaa	atttagagag	ggggtataat	atgaacgaag
8401	taaaattcag	atttacagac	tcagaagcgt	ttcacatgtt	tatatacgtc	ggggatttaa
8461	aattactcta	ctttttat	gtattaatgt	tcgttgatat	tattacaggt	atttcaaaag
8521	caattaaaaa	taataactta	tggtcaaaaa	aatcaatgag	aggattttct	aaaaaattat
8581	tgatattctg	tattatcatt	ttagcaaaaca	tcattgacca	gatttttaca	ttaaaagggtg
8641	gtctactcat	gattacaata	ttttattata	ttgcaaatga	gggactttct	attgtagaaa
8701	attgtgcaga	aatggacgta	ttagtaccag	aacaaattaa	agataaatta	agagtcatta
8761	aaaatgatac	tgaaaagagt	gataacaatg	aacgatcaag	agaagataga	taaatttacg
8821	cattcctata	ttaatgatga	ttttgggtta	acgatagacc	agtttagtccc	taaagtaaaa
8881	ggatatgggc	gctttaatgt	atggcttggt	ggtaatgaaa	gtaaaatcag	acaagtatta
8941	aaagcagtaa	aagagatagg	tgtttcacct	actctttttg	ccgtatatga	aaaaaatgag
9001	ggtttttagtt	ctggacttgg	ttgggttaaac	catacgtctg	cacgtgggtga	ttatttaaca
9061	gatgctaaat	tcatagcaag	aaagtttagta	tcacaatcaa	aacaagctgg	acaaccgtct
9121	tggtatgacg	caggtaacat	cgtccacttt	gtaccacaag	acgtacaaag	aaaaggtaat
9181	gcagattttg	caaaaaatat	gaaagcaggt	acaattggac	gtgcatatat	tccattaaca
9241	gcagctgcta	cttgggcggc	atattatcct	ttagggtttga	aagcatcata	taacaaagta
9301	caaaactatg	gtaatccatt	tttagacgggt	gcgaatacta	ttctagcttg	gggtggtaaa
9361	ttagacggta	aagggtggatc	acctagtgat	tcgtctgaca	gtggtagtag	tggtgacagt

TABLE 1

9421	ggtagttcac	tactcgcttt	agcaaaacaa	gccatgcaag	aattattaaa	aaaaatacaa
9481	gacgcattac	aatgggacgt	tcatagtatt	ggtagtgata	aatTTTTtag	taatgattat
9541	tttacattag	aaaaaacatt	taacaacaca	tatcatatta	aaatgacgat	tggtttactt
9601	gattcattaa	aaaaactgat	tgatagcggt	caagtagata	gtgggagtag	tagttcctaat
9661	cctactgatg	atgacggaga	ccataaacca	attagtggta	aatcagtcac	gccaaatgga
9721	aaaagtggtc	gtgtgattgg	tggtaactgg	acatatgcac	agttaccaga	aaaatataaa
9781	aaagcaattg	gtgtaccttt	attcaaaaaa	gaatacttat	acaaaccagg	taacatatTT
9841	cctcaaacgg	gtaatgcagg	acaatgtaca	gaattaacat	gggcgtatat	gtcacaacta
9901	catggtaaaa	gacaacctac	cgacgacggg	caaataacaa	acggtcagcg	tgtatgggtac
9961	gtctataaaa	agtttaggtg	aaaaacaaca	cataatccaa	cagtaggtta	tggtttctct
10021	agtaaaccac	catacttaca	agcaactgca	tatgggtattg	gtcacacagg	tgttggtgta
10081	gcagtttttg	aagatgggtc	gttttttagtt	gcaaaactata	atgtaccacc	atatgttgca
10141	ccatcacgtg	tggtattgta	tacactcatt	aatggcgtag	caaataatgc	tggtgataat
10201	attgtattct	ttagtgggtat	tgcttaatta	actatgctat	aatgaacaca	tgctagtaat
10261	gctagtaaat	aaaatacaaa	acataatcaa	ttttcgtaca	catttttcat	gttatctcaa
10321	aaagaaaagg	agactgttat	tttaacagtt	gccttttttt	atttcatcat	gttcacgttt
10381	taatatatgc	aaatcagatt	tgttatgtac	tgaacgttca	actggaaata	agtcgttaag
10441	tgaaaatgaa	ccgatgtcac	tttcaatata	agaatatca	tcaaattgac	tatggtcgaa
10501	attttctcta	gcgtctttta	atataaatTC	acgtttcata	ttaagttcat	cagtaaaata
10561	ttcatcatat	acattaccac	atacaatttc	agtttttagac	ggatatatcg	atattgtacc
10621	ttgctcatta	tagatacttt	tattgttttc	aataatggca	cogtcaaaga	attgttcacg
10681	tacaaagggt	tcaaaatcga	cgcttgatc	aaaggcggtt	ttcgggtatac	cagcagaagc
10741	aatttttaate	tttccattca	cttcatatgc	atatttctta	tgattcagta	caaacatctt
10801	atctatctgt	tcgtttttcaa	tatcccattt	acctaaggct	atcgggtcga	ataaactggg
10861	gttcaataag	ggtttaacaa	cggtattcat	atacaaaacta	tcagtatcgc	aataaataaa
10921	attgtcgtca	atttcacttt	cogttaagta	ttggaaagga	accaataagt	tatacaatga
10981	acgtgatgtg	acaaatgtag	agaataatat	attacgttca	gtgtttttgt	aaccgttaat
11041	gatattgtat	agttcattgt	tatcatctaa	acggaataag	ttaaaatgtg	aacgtaatgc
11101	aggatgcca	tataatccat	ttaaaacgac	tttagataac	ataacctcct	catttgagta
11161	tgggtgttcg	ttgatatcat	cagtaatgtg	atagtcgtaa	ggatgatgtca	tattgatttt
11221	gttttttaac	ttaccttggtg	ttttaataaa	atagttttga	aaaataatat	cacgtgcatg
11281	aaagtattca	cattcatata	taacaaacga	attaacacgt	atatgcatgc	aatcaatacc
11341	cgtaatgtct	tgaatcattc	ttaatgtatt	tgtattgata	ttaacgtaat	cattatcatt
11401	attatagtat	tttacaatca	tttgacgtaa	tacacgtgat	ttaatTTtaa	ttataaaatc
11461	atcgttaaat	acatctttat	caatcttata	taatgaaaaa	taattgtcat	catctaaaaa
11521	agtagggatt	aacgttggtt	ctgaatagtg	ttcgtaaaag	tataaccatg	ttggaatttt
11581	ttcatgatac	atcacataag	gataactcga	attgatgtca	atagaaaaac	aaggctcatc
11641	aattagtttg	tttatgtatt	tggtgttata	catattttaa	ccaccacgat	agaatgattt
11701	aatatagtca	taaaaattca	tatcatggaa	atgataatgt	gtataagata	ttttaatatc
11761	ttgatattgg	ttgagtaact	gaaaacgtgt	catttcatta	ttcaagtaag	attccataat
11821	attcaatgaa	aatgttaatt	tgttatagtc	aaaatttgga	aatatatcac	tataatgaat
11881	atggcacata	cctaataata	tcacgtcatt	atgaatgtat	gtaagttggt	cagggtgtgag
11941	ttttgcaaaa	catttcacag	catagtcata	ggcttcacta	tcattcatat	cattatcttt
12001	atcaaaaate	gtataattaa	aatctgtttt	aagttgtgat	tctgttaaat	aaccaccatc
12061	aagtaatttc	ttacctaatg	ttgcaattga	tgtattgggt	ttcataaagt	tatcaataat
12121	attaaattta	aaaccattta	aaaacattgt	taaatctaaa	ttgattgaag	atttaacacg
12181	tttttctaaa	attacatttt	gatttttggtc	taaaatagta	gcctctttca	tttttaatgt
12241	gtgttcattt	tcttctgcag	atttttaata	tatattttcg	cgtgtaatat	tatcaaaata
12301	acgcatgggtg	tctttaagta	aaaaatgatt	atcgtattta	ttacagttat	gtgcaatcat
12361	gataatatct	gtttttgatt	ttgtgattgt	atcacgtctt	ttcacatacg	tataaaatgc
12421	gtcataaaaa	gattcgaaac	tcggaaatac	ttcaacatca	atttcataac	cattaaacca
12481	accaattgct	acagaataag	taacgttttt	atatttggtt	gggttttttc	gtcogttaac
12541	tttattgtac	gctaattggtt	ctatatccca	gtataaaatc	attcgacgtt	catgtttatg

GCTT = 262260

TABLE 1

12601	atattgcatg	cattctagta	atcccataat	cttacacacc	ttttataagc	catattgttt
12661	cattagatac	tttttcgtat	tctctatata	gttatcttcg	tatatttttt	cttttccttc
12721	aaactcactc	atatttttct	tcatttccatt	ttttatatga	aattttataa	ttttattcat
12781	atctaaatat	aaatatctat	cattatcaac	cacgtaattt	ttagagtaag	cattgtcaaa
12841	atgtaaattg	cttggattgt	agtaataacg	ttccatgttt	tctttataaa	acatatcatc
12901	acgtaaatag	gtaacatgat	tgtctatatc	cctaatttta	gtacaaaatt	catattgttt
12961	tgtatatggg	acaacgataa	tatttgtcat	aaaagtagtt	acattataca	tgactttaat
13021	atattttatca	tcagttttga	tatagaagaa	atcacggttt	tgattgatgt	gatttcttaa
13081	attatcatcc	gccaaattat	attcgttaaa	ttcaaattct	ccagttgtca	tagcgtcgtc
13141	atttgaatta	aacgcacgtg	tgttacgttt	ttcattcacg	taatcgtttc	gtcgcatctc
13201	taaaaaaatg	tttttgtaaa	gtcttgatgt	attcatttta	tgcttttgta	ataaattgta
13261	tatattttaa	ttggataata	taggacttga	aaagttgact	gcattaccta	gtaaaaacat
13321	tttaggggaat	ccaatataat	caacgttacc	atggttacgg	tcgattgatt	catatatgtt
13381	ttttaactta	tcccactcat	caattaaata	atcatcttca	agtgtctaaa	actcatcata
13441	tataataata	ggatagtgtt	ttaaaaagtt	agaatgatat	tttaaatacag	tggcactatt
13501	caaactctgta	atcacaccaa	tttctttatc	ttgatagata	atagctaaat	agtccttagc
13561	acttctgaac	gtgacacgtt	ttgattttaa	tagtggattt	tcattctatga	tttcttcaat
13621	aaaatcacgg	taagcgtcac	gtaatgtata	atgacgtgat	aataaagtaa	attttatatc
13681	aagtttaata	gctaaataaa	taaaaaatga	aacatagttg	aacgattttc	catcagaacg
13741	gtttgaaata	gatataataa	aatctatatc	atcattcata	agttcatcaa	ctaattctat
13801	ttgattatac	ttatctggga	ttttttttct	gacatgattg	acagcatttt	gataatctct
13861	taccatgtct	aaacgatttt	gttttaccat	gtttttgctc	cttgtaatag	tttatgatgt
13921	cgtttacagt	gttaaattta	ttcgtcaaat	gttgcataat	ataaaaagtt	atacctcaca
13981	tcttcatcat	caatatttgt	cactgggtcta	tctgatttac	caatttcttt	atataaagta
14041	tcgatttctt	taatatattt	atacattgaa	gaattattat	ttttagcttg	taaatttatat
14101	aaagcgtatt	tatgcttttt	agcgttttta	ttattagaat	catcattacg	gttatatatt
14161	tcaagaatat	aatttaattt	tttatgtctt	gaacctctta	ccaatgatac	agcattttaca
14221	tatgatacgt	ttctttcttt	aggaaaatag	ggcagatgtg	caaaatgttt	ccatgtgtca
14281	atgtacgcct	cttgtaaatc	tttatcatca	aattttaaaat	taacattact	aaaatcattt
14341	aaaaataaat	ctttttcttg	ctcttttcta	gcttctcttt	cttttttcca	tctatccatt
14401	tcagacgtat	gtctaaccaa	tgttatcaac	ctccatataa	agcataaata	accattaaaa
14461	agataatata	gaatataatc	aatgtagtga	ataaaacacc	aaatgacacg	cgtatatgca
14521	gtgtcataag	tatgataagt	gtaattaaaa	atgctaaaag	gaaaacaatg	gctatgttta
14581	ataggttatt	catgggtcaat	cactttccca	ttatcgtata	tgactttggt	ttgataaata
14641	atcattaatt	cgctttcaag	aggtttatca	aaatttgata	atacgtcgtc	aatttgtaacg
14701	tttaataaaa	tttctcttat	taattcatta	cttaaataat	ttctataata	aaatacaagt
14761	atattaaaaa	catgtttttt	aatatcaatg	tcgatatacta	acgtaaaata	ctctttttca
14821	atttcaaaaat	catcatattg	tttgtcaaac	tcaatatata	catcaccocat	atttattttt
14881	actatacatt	ttttattaga	tgaagtaaat	ttttcaaatt	tatcattata	ataatctcta
14941	tttgttaaaa	ggtaataaat	taaattattt	aatctaaaag	tagttttaat	tttcattttt
15001	atatctcctt	aatgtattct	atgatatacg	cgtatttttt	agtgaacagg	ttatattcat
15061	aatatgaata	tacaacttta	gogtcatata	aatcttcaaa	cattgagatt	tgatgtggaa
15121	aatgtccttt	aatctcatcg	caatataata	ataccgtttt	gtatttacgt	tccattttaa
15181	cacctcataa	aaaatagggg	ataagtatcc	cctatgaaat	tgtattaaaa	tgatacttga
15241	ccaaaattga	ttgagtaacc	tttttgacct	tttttgtttt	catattcata	aattgtgaat
15301	tgaacttctc	cagcattgat	aatgtcaaca	acgtctctcat	ctgctctcat	ttctttaatt
15361	aattctgtta	agtgggtcgg	taagtttacg	ttatagtcac	cagtgaacgat	aacaccttgt
15421	tcaccgaatt	ttgattcttt	gtttgtgaat	aatgctctaa	cgatatactc	ttttttcata
15481	cgtatttttt	ctactaattc	tgatagtttg	ataaattctc	tttctttttc	ctcaaattca
15541	aatctcgtca	atgtgttttg	gtgtcttgat	aaaatatctt	ttacgtttgt	catttttatt
15601	ctctctttat	ttaaattatt	tgctttctgc	aattgcgatt	tgtagtaaat	catttgtaata
15661	aacttgaatt	gttttcgttg	tgcgtgtagt	ggacaatagt	ttacatgtgt	ctggtaataa
15721	ttctttttgct	tgtgttttgg	ttaaatgata	ctcgtgaagt	ggtaaaaatt	cctcaatgta

TABLE 1

15781	ttcattatca	tcatctaagt	aatgaagtat	ataacctttg	acacgtaagg	taacaatgtc
15841	gtcaactttc	attattatat	cactcctttc	taaaaaacgt	aaacgttata	cgtttcataa
15901	aatcctttat	gcatattcca	ttgttctatt	gggtcatcac	cagcaatata	agacaatatt
15961	gattctgggt	tagtttcggt	gtttagttca	tcatttaaga	attgaacaac	agaactatta
16021	tagtttaata	atagttggtg	gcaagccgat	aataagttaa	ttgcattgtc	aatgtataa
16081	gctggattcc	attgaatcag	tttattgaat	agttgcaaca	tttcagtata	ggcttgtcct
16141	ttttcttctg	gtgcattatc	aacattaacc	attattatca	cttctaata	aagttgaaat
16201	tacgcgtaaa	acagaattat	gatttaaata	ttcaatttca	tcaatgtcaa	catcataaaa
16261	tgaaatttca	ttttctgttc	tatcaaataa	cgctatacat	aaacttccat	tcttaaaacg
16321	aaaaacatgc	ttcaactcaa	tgttttttgt	ttcattttcc	atttttgtta	ctccttgttt
16381	tgattacata	cttagtatag	caaacgttta	aaagttttgt	caatagtttt	tcttaaaaaa
16441	gtttaaataa	ttttaaaact	actatttaat	agaagaaata	agattttaag	ttcaaatacat
16501	aattttgaat	aaaagtcaat	agatacataa	attttgtatt	tgatgaatat	gtaatagggt
16561	agataagttg	gttaagttgt	tgcacagtat	ttttaagttt	agtaaagaaa	tgataagtaa
16621	atttataagt	tttgatttgt	ataatcgttt	attttaaacc	ggtggggt	

15781 15841 15901 15961 16021 16081 16141 16201 16261 16321 16381 16441 16501 16561 16621

TABLE 2

1st position (5' end)	2nd position				3rd position (3' end)
	U	C	A	G	
U	Phe	Ser	Tyr	Cys	U
	Phe	Ser	Tyr	Cys	C
	Leu	Ser	Stop	Stop	A
	Leu	Ser	Stop	Trp	G
C	Leu	Pro	His	Arg	U
	Leu	Pro	His	Arg	C
	Leu	Pro	Gln	Arg	A
	Leu	Pro	Gln	Arg	G
A	Ile	Thr	Asn	Ser	U
	Ile	Thr	Asn	Ser	C
	Ile	Thr	Lys	Arg	A
	Met	Thr	Lys	Arg	G
G	Val	Ala	Asp	Gly	U
	Val	Ala	Asp	Gly	C
	Val	Ala	Glu	Gly	A
	Val	Ala	Glu	Gly	G

007027 232260

TABLE 3

44AHJDORF012, Nucleotides and amino acids sequences

8391 atgaacgaagtaaaattcagatttacagactcagaagcggtttcac
1 M N E V K F R F T D S E A F H
8436 atgtttatatacgctggggattttaaattactctactttttattt
16 M F I Y A G D L K L L Y F L F
8481 gtattaatgttcggttgatattattacaggtatttcaaagcaatt
31 V L M F V D I I T G I S K A I
8526 aaaaataataacttatgggtcaaaaaaatcaatgagaggattttct
46 K N N N L W S K K S M R G F S
8571 aaaaaattattgatattctgtattatcatttttagcaaacatcatt
61 K K L L I F C I I I L A N I I
8616 gaccagattttacaattaaaagggtggtctactcatgattacaata
76 D Q I L Q L K G G L L M I T I
8661 ttttattatattgcaaattgagggactttctattgtagaaaattgt
91 F Y Y I A N E G L S I V E N C
8706 gcagaaatggacgtatttagtaccagaacaaattaaagataaatta
106 A E M D V L V P E Q I K D K L
8751 agagtcattaaaaatgatactgaaaagagtgataacaatgaacga
121 R V I K N D T E K S D N N E R
8796 tcaagagaagatagataa 8813
136 S R E D R *

44AHJDORF025, Nucleotides and amino acids sequences

15175 atggaacgtaaatacaaaacggtattattatattgcatgagatt
1 M E R K Y K T V L L Y C D E I
15130 aaaggacattttccacatcaaattctcaatgtttgaagatttatat
16 K G H F P H Q I S M F E D L Y
15085 gacgctaaagttgtatattcatattatgaatataacctgttcact
31 D A K V V Y S Y Y E Y N L F T
15040 aaaaaatacgcgatatatcatagaatacattaaggagatataa 14999
46 K K Y A Y I I E Y I K E I *

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[illegible]

Sequences producing significant alignments:	Score (bits)	E Value
sp P52869 EAEA_HAFAL INTIMIN (OUTER MEMBRANE PROTEIN) (ATTACHI...	28	1.9
sp Q02785 PDRC_YEAST ATP-DEPENDENT PERMEASE PDR12.	27	4.2
sp P75252 Y350_MYCPN HYPOTHETICAL PROTEIN MG350 HOMOLOG.	27	5.6
sp P41665 Y112_NPVAC HYPOTHETICAL 10.5 KD PROTEIN IN HE65-PK2 ...	27	5.6
sp P26744 VG01_BPP22 PORTAL PROTEIN (PROTEIN GP1).	26	7.3
sp P36542 ATPG_HUMAN ATP SYNTHASE GAMMA CHAIN, MITOCHONDRIAL P...	26	9.5
sp P35435 ATPG_RAT ATP SYNTHASE GAMMA CHAIN, MITOCHONDRIAL (EC...	26	9.5

TABLE 5

Physico-chemical parameters for 44AHJDORF012

1 MNEVKFRFTD SEAFHMFIIYA GDLKLLYFLF VLMFVDIITG ISKAIKNNNL WSKKSMRGFS
 61 KLLIFCIII LANIIDQILQ LKGGLLMITI FYYIANEGLS IVENCAEMDV LVPEQIKDKL
 121 RVIKNDTEKS DNNERSREDR

Number of amino acids: 140
 Average molecular weight (Daltons): 16294.30
 Mean amino acid weight (Daltons): 116.39
 Monoisotopic molecular weight (Daltons): 16283.58
 Mean amino acid monoisotopic weight (Daltons): 116.31

Amino acid composition

Acid	Symbol	Number	%	Average % in Swissprot	Acid	Symbol	Number	%	Average % in Swissprot
Ala	A	6	4.29%	7.58%	Cys	C	2	1.43%	1.66%
Asp	D	9	6.43%	5.28%	Glu	E	9	6.43%	6.37%
Phe	F	10	7.14%	4.09%	Gly	G	6	4.29%	6.84%
His	H	1	0.71%	2.24%	Ile	I	18	12.86%	5.81%
Lys	K	13	9.29%	5.95%	Leu	L	16	11.43%	9.42%
Met	M	6	4.29%	2.37%	Asn	N	10	7.14%	4.45%
Pro	P	1	0.71%	4.9%	Gln	Q	3	2.14%	3.97%
Arg	R	6	4.29%	5.16%	Ser	S	8	5.71%	7.12%
Thr	T	4	2.86%	5.67%	Val	V	7	5.00%	6.58%
Trp	W	1	0.71%	1.23%	Tyr	Y	4	2.86%	3.18%

Number of acidic (negative) amino acids (ED): 18 12.86%
 Number of basic (positive) amino acids (KR): 19 13.57%
 Total charge (KRED): 37 26.43%
 Net charge (KR - ED): 1 0.71%
 Theoretical pI: 8.16
 Total linear charge density: 0.28
 Average hydrophobicity: 1.26
 Ratio of hydrophilicity to hydrophobicity: 0.92
 Percentage of hydrophilic amino acid: 45.71%
 Percentage of hydrophobic amino acid: 54.29%
 Ratio of %hydrophilic to %hydrophobic: 0.84

Hydrophobicity plot

Kyte-Doolittle scale

Ala: 1.800 Arg: -4.500 Asn: -3.500
 Asp: -3.500 Cys: 2.500 Gly: -0.400
 Gln: -3.500 Glu: -3.500 His: -3.200
 Ile: 4.500 Leu: 3.800 Lys: -3.900
 Met: 1.900 Phe: 2.800 Pro: -1.600
 Ser: -0.800 Thr: -0.700 Trp: -0.900
 Tyr: -1.300 Val: 4.200

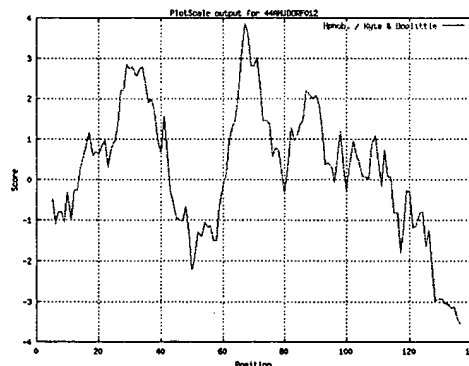


TABLE 5

Physico-chemical parameters for 44AHJDORF025

1 MERKYKTVLL YCDEIKGHFP HQISMFEDLY DAKVVYSYIE YNLFTKKYAY IIEYIKEI

Number of amino acids: 58
Average molecular weight (Daltons): 7248.41
Mean amino acid weight (Daltons): 124.97
Monoisotopic molecular weight (Daltons): 7243.60
Mean amino acid monoisotopic weight (Daltons): 124.89

Amino acid composition

Acid	Symbol	Number	%	Average % in Swissprot	Acid	Symbol	Number	%	Average % in Swissprot
Ala	A	2	3.45%	7.58%	Cys	C	1	1.72%	1.66%
Asp	D	3	5.17%	5.28%	Glu	E	6	10.34%	6.37%
Phe	F	3	5.17%	4.09%	Gly	G	1	1.72%	6.84%
His	H	2	3.45%	2.24%	Ile	I	6	10.34%	5.81%
Lys	K	7	12.07%	5.95%	Leu	L	4	6.90%	9.42%
Met	M	2	3.45%	2.37%	Asn	N	1	1.72%	4.45%
Pro	P	1	1.72%	4.9%	Gln	Q	1	1.72%	3.97%
Arg	R	1	1.72%	5.16%	Ser	S	2	3.45%	7.12%
Thr	T	2	3.45%	5.67%	Val	V	3	5.17%	6.58%
Trp	W	0	0.00%	1.23%	Tyr	Y	10	17.24%	3.18%

Number of acidic (negative) amino acids (ED): 9 15.52%
Number of basic (positive) amino acids (KR): 8 13.79%
Total charge (KRED): 17 29.31%
Net charge (KR - ED): -1 -1.72%
Theoretical pI: 6.08
Total linear charge density: 0.33

Average hydrophobicity: -3.72
Ratio of hydrophilicity to hydrophobicity: 1.30
Percentage of hydrophilic amino acid: 44.83%
Percentage of hydrophobic amino acid: 55.17%
Ratio of %hydrophilic to %hydrophobic: 0.81

Hydrophobicity plot

Kyte-Doolittle scale

Ala: 1.800 Arg: -4.500 Asn: -3.500
Asp: -3.500 Cys: 2.500 Gly: -0.400
Gln: -3.500 Glu: -3.500 His: -3.200
Ile: 4.500 Leu: 3.800 Lys: -3.900
Met: 1.900 Phe: 2.800 Pro: -1.600
Ser: -0.800 Thr: -0.700 Trp: -0.900
Tyr: -1.300 Val: 4.200

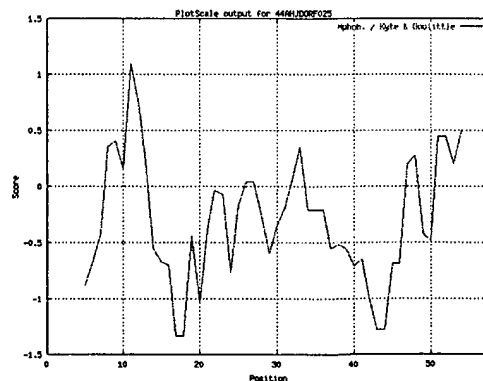


TABLE 6

>gi|11094395|gb|AAG29618.1| integrase-like protein [Staphylococcus aureus]
>gi|11094394|gb|AAG29617.1|AF217235_20 Orf20 [Staphylococcus aureus]
>gi|11094393|gb|AAG29616.1|AF217235_19 Orf19 [Staphylococcus aureus]
>gi|11094392|gb|AAG29615.1|AF217235_18 Orf18 [Staphylococcus aureus]
>gi|11094391|gb|AAG29614.1|AF217235_17 Orf17 [Staphylococcus aureus]
>gi|11094390|gb|AAG29613.1|AF217235_16 Orf16 [Staphylococcus aureus]
>gi|11094389|gb|AAG29612.1|AF217235_15 Orf15 [Staphylococcus aureus]
>gi|11094388|gb|AAG29611.1|AF217235_14 Orf14 [Staphylococcus aureus]
>gi|11094387|gb|AAG29610.1|AF217235_13 Orf13 [Staphylococcus aureus]
>gi|11094386|gb|AAG29609.1|AF217235_12 Orf12 [Staphylococcus aureus]
>gi|11094385|gb|AAG29608.1|AF217235_11 Orf11 [Staphylococcus aureus]
>gi|11094384|gb|AAG29607.1|AF217235_10 Orf10 [Staphylococcus aureus]
>gi|11094383|gb|AAG29606.1|AF217235_9 Orf9 [Staphylococcus aureus]
>gi|11094382|gb|AAG29605.1|AF217235_8 Orf8 [Staphylococcus aureus]
>gi|11094381|gb|AAG29604.1|AF217235_7 Orf7 [Staphylococcus aureus]
>gi|11094380|gb|AAG29603.1|AF217235_6 Orf6 [Staphylococcus aureus]
>gi|11094379|gb|AAG29602.1|AF217235_5 Orf5 [Staphylococcus aureus]
>gi|11094378|gb|AAG29601.1|AF217235_4 toxic shock syndrome toxin-1 [Staphylococcus aureus]
>gi|11094377|gb|AAG29600.1|AF217235_3 Orf3 [Staphylococcus aureus]
>gi|11094376|gb|AAG29599.1|AF217235_2 staphylococcal enterotoxin C-bovine [Staphylococcus aureus]
>gi|11094375|gb|AAG29598.1|AF217235_1 sel [Staphylococcus aureus]
>gi|9944978|gb|AAG03058.1|AF288215_5 response regulator [Staphylococcus aureus]
>gi|9944977|gb|AAG03057.1|AF288215_4 receptor histidine kinase [Staphylococcus aureus]
>gi|9944976|gb|AAG03056.1|AF288215_3 Agr autoinducing peptide precursor [Staphylococcus aureus]
>gi|9944975|gb|AAG03055.1|AF288215_2 putative AIP processing-secretion protein [Staphylococcus aureus]
>gi|9944974|gb|AAG03054.1|AF288215_1 delta hemolysin [Staphylococcus aureus]
>gi|10956173|ref|NP_048342.1| ORF64 [Staphylococcus aureus]
>gi|10956172|ref|NP_048341.1| replication protein [Staphylococcus aureus]
>gi|10956170|ref|NP_048340.1| ORF64 [Staphylococcus aureus]
>gi|10956169|ref|NP_048339.1| replication protein [Staphylococcus aureus]
>gi|10956167|ref|NP_052696.1| pot. orfB (aa 1-92) (4557 is 2nd base in codon) [Staphylococcus aureus]
>gi|10956166|ref|NP_052695.1| pot. orfA [Staphylococcus aureus]
>gi|10956165|ref|NP_052694.1| CAT gene (aa 1-215) [Staphylococcus aureus]
>gi|10956164|ref|NP_052693.1| repD (aa 1-311) [Staphylococcus aureus]
>gi|10956163|ref|NP_052692.1| unidentified reading frame [Staphylococcus aureus]
>gi|10956161|ref|NP_052691.1| kanamycin nucleotidyltransferase (AA 1-253) [Staphylococcus aureus]
>gi|10956160|ref|NP_052690.1| repB polypeptide (AA 1-235) [Staphylococcus aureus]
>gi|10956158|ref|NP_052168.1| recombination protein [Staphylococcus aureus]
>gi|10956157|ref|NP_052167.1| CAT protein [Staphylococcus aureus]
>gi|10956156|ref|NP_052166.1| replication protein [Staphylococcus aureus]
>gi|10956154|ref|NP_053794.1| replication protein [Staphylococcus aureus]
>gi|10956153|ref|NP_053796.1| recombination protein [Staphylococcus aureus]
>gi|10956152|ref|NP_053795.1| tetracycline resistance protein [Staphylococcus aureus]
>gi|10956150|ref|NP_052130.1| beta-lactamase [Staphylococcus aureus]
>gi|10956148|ref|NP_052129.1| beta-lactamase [Staphylococcus aureus]
>gi|10956146|ref|NP_044360.1| tetracycline resistance protein [Staphylococcus aureus]
>gi|10956145|ref|NP_044359.1| replication protein [Staphylococcus aureus]
>gi|10956143|ref|NP_040438.1| reading frame D [Staphylococcus aureus]
>gi|10956142|ref|NP_040437.1| CAT (chloramphenicol resistance) [Staphylococcus aureus]
>gi|10956141|ref|NP_040435.1| reading frame A [Staphylococcus aureus]
>gi|10956140|ref|NP_040436.1| reading frame C (replication) [Staphylococcus aureus]
>gi|10946545|gb|AAG23889.1| TcaB [Staphylococcus aureus]
>gi|10946544|gb|AAG23888.1| TcaA [Staphylococcus aureus]
>gi|10946543|gb|AAG23887.1| TcaR [Staphylococcus aureus]
>gi|2792490|gb|AAB97073.1| coenzyme A disulfide reductase [Staphylococcus aureus]
>gi|10835501|pdb|1D2P|A Chain A, Crystal Structure Of Two B Repeat Units (B1b2) Of The Collagen Binding Protein (Cna) Of Staphylococcus Aureus
>gi|10835500|pdb|1D20|B Chain B, Crystal Structure Of A Single B Repeat Unit (B1) Of Collagen Binding Surface Protein (Cna) Of Staphylococcus Aureus.
>gi|10835499|pdb|1D20|A Chain A, Crystal Structure Of A Single B Repeat Unit (B1) Of Collagen Binding Surface Protein (Cna) Of Staphylococcus Aureus.
>gi|1169372|sp|P45555|DNAJ_STAAU CHAPERONE PROTEIN DNAJ (HSP40)
>gi|7672995|gb|AAF66692.1|AF144682_1 immunodominant antigen B [Staphylococcus aureus]
>gi|7672993|gb|AAF66691.1|AF144681_1 immunodominant antigen A [Staphylococcus aureus]
>gi|9955268|pdb|1QE0|B Chain B, Crystal Structure Of Apo S. Aureus Histidyl-Trna Synthetase
>gi|9955267|pdb|1QE0|A Chain A, Crystal Structure Of Apo S. Aureus Histidyl-Trna Synthetase

>gi|9711533|dbj|BAB07837.1| coagulase [Staphylococcus aureus]
>gi|9711528|dbj|BAB07836.1| coagulase [Staphylococcus aureus]
>gi|9711524|dbj|BAB07835.1| coagulase [Staphylococcus aureus]
>gi|9711520|dbj|BAB07834.1| coagulase [Staphylococcus aureus]
>gi|9711516|dbj|BAB07833.1| coagulase [Staphylococcus aureus]
>gi|9711512|dbj|BAB07832.1| coagulase [Staphylococcus aureus]
>gi|9711508|dbj|BAB07831.1| coagulase [Staphylococcus aureus]
>gi|9711504|dbj|BAB07830.1| coagulase [Staphylococcus aureus]
>gi|9711500|dbj|BAB07829.1| coagulase [Staphylococcus aureus]
>gi|9711496|dbj|BAB07828.1| coagulase [Staphylococcus aureus]
>gi|9711492|dbj|BAB07827.1| coagulase [Staphylococcus aureus]
>gi|9711488|dbj|BAB07826.1| coagulase [Staphylococcus aureus]
>gi|9711484|dbj|BAB07825.1| coagulase [Staphylococcus aureus]
>gi|9711480|dbj|BAB07824.1| coagulase [Staphylococcus aureus]
>gi|9622622|gb|AAF89877.1| putative site-specific recombinase XerC [Staphylococcus aureus]
>gi|9622620|gb|AAF89876.1| putative site-specific recombinase XerD [Staphylococcus aureus]
>gi|3806109|gb|AAC69195.1| HsdM-like protein [Staphylococcus aureus]
>gi|3806108|gb|AAC69194.1| exotoxin 4 [Staphylococcus aureus]
>gi|3806107|gb|AAC69193.1| exotoxin 5 [Staphylococcus aureus]
>gi|3806106|gb|AAC69192.1| exotoxin 1 [Staphylococcus aureus]
>gi|3806105|gb|AAC69191.1| exotoxin 3 [Staphylococcus aureus]
>gi|3806104|gb|AAC69190.1| exotoxin 2 [Staphylococcus aureus]
>gi|6176434|gb|AAF05589.1|AF188837_1 exotoxin 1 [Staphylococcus aureus]
>gi|6176433|gb|AAF05588.1|AF188836_1 exotoxin 1 [Staphylococcus aureus]
>gi|6176432|gb|AAF05587.1|AF188835_1 exotoxin 1 [Staphylococcus aureus]
>gi|9501795|dbj|BAB03342.1| Protein A [Staphylococcus aureus]
>gi|9501794|dbj|BAB03341.1| hyothetical protein [Staphylococcus aureus]
>gi|9501793|dbj|BAB03340.1| hypothetical protein [Staphylococcus aureus]
>gi|9501791|dbj|BAB03339.1| ABC transporter [Staphylococcus aureus]
>gi|9501790|dbj|BAB03338.1| ABC transporter [Staphylococcus aureus]
>gi|9501788|dbj|BAB03337.1| ABC transporter [Staphylococcus aureus]
>gi|9501787|dbj|BAB03336.1| ABC transporter [Staphylococcus aureus]
>gi|9501785|dbj|BAB03335.1| hypothetical protein [Staphylococcus aureus]
>gi|9501784|dbj|BAB03334.1| hypothetical protein [Staphylococcus aureus]
>gi|9501783|dbj|BAB03333.1| hypothetical protein [Staphylococcus aureus]
>gi|9501781|dbj|BAB03332.1| fructose specific permease [Staphylococcus aureus]
>gi|9501780|dbj|BAB03331.1| fructose 1-phosphate kinase [Staphylococcus aureus]
>gi|9501779|dbj|BAB03330.1| fru operon repressor [Staphylococcus aureus]
>gi|9501777|dbj|BAB03329.1| hypothetical protein [Staphylococcus aureus]
>gi|9501776|dbj|BAB03328.1| acetyl-CoA c-acetyltransferase [Staphylococcus aureus]
>gi|9501775|dbj|BAB03327.1| long chain fatty acid CoA ligase [Staphylococcus aureus]
>gi|9501774|dbj|BAB03326.1| Pro/Bet transporter homolog [Staphylococcus aureus]
>gi|9501772|dbj|BAB03325.1| response regulator [Staphylococcus aureus]
>gi|9501771|dbj|BAB03324.1| histidine kinase sensor [Staphylococcus aureus]
>gi|9501770|dbj|BAB03323.1| hypothetical protein [Staphylococcus aureus]
>gi|9501769|dbj|BAB03322.1| hypothetical protein [Staphylococcus aureus]
>gi|9501768|dbj|BAB03321.1| methionin aminopeptidase [Staphylococcus aureus]
>gi|9501767|dbj|BAB03320.1| hypothetical protein [Staphylococcus aureus]
>gi|7328282|emb|CAB82465.1| catabolite control protein A [Staphylococcus aureus]
>gi|9408171|emb|CAA71131.1| ORF213 [Staphylococcus aureus]
>gi|9408170|emb|CAA71130.1| ORF133 [Staphylococcus aureus]
>gi|9408169|emb|CAA71129.1| aldehyde dehydrogenase [Staphylococcus aureus]
>gi|8895763|gb|AAF81096.1|AF228662_1 putative undecaprenol kinase [Staphylococcus aureus]
>gi|8777467|dbj|BAA97049.1| 29-kDa cell surface protein [Staphylococcus aureus]
>gi|7328286|emb|CAB82467.1| diaminopimelate decarboxylase [Staphylococcus aureus]
>gi|581546|emb|CAA36783.1| AgrB protein [Staphylococcus aureus]
>gi|581545|emb|CAA36781.1| hypothetical protein [Staphylococcus aureus]
>gi|46600|emb|CAA37901.1| putative transposase [Staphylococcus aureus]
>gi|46599|emb|CAA37900.1| putative transposase [Staphylococcus aureus]
>gi|46513|emb|CAA36786.1| hypothetical protein [Staphylococcus aureus]
>gi|46512|emb|CAA36785.1| hypothetical protein [Staphylococcus aureus]
>gi|46511|emb|CAA36784.1| AgrA protein [Staphylococcus aureus]
>gi|46509|emb|CAA36782.1| hypothetical protein [Staphylococcus aureus]
>gi|46507|emb|CAA36780.1| Hld protein [Staphylococcus aureus]
>gi|46506|emb|CAA36779.1| hypothetical protein [Staphylococcus aureus]
>gi|9256926|pdb|1D6E|C Chain C, Crystal Structure Of Hla-Dr4 Complex With Peptidomimetic And Seb
>gi|9256923|pdb|1D5Z|C Chain C, X-Ray Crystal Structure Of Hla-Dr4 Complexed With Peptidomimetic And Seb
>gi|9256920|pdb|1D5X|C Chain C, X-Ray Crystal Structure Of Hla-Dr4 Complexed With Dipeptide Mimetic And Seb
>gi|9256852|pdb|1D5M|C Chain C, X-Ray Crystal Structure Of Hla-Dr4 Complexed With Peptide And Seb

>gi|8569412|pdb|1DEE|H Chain H, Crystal Structure At 2.7a Resolution Of A Complex Between A Staphylococcus Aureus Domain And A Fab Fragment Of A Human Igm Antibody
>gi|8569411|pdb|1DEE|G Chain G, Crystal Structure At 2.7a Resolution Of A Complex Between A Staphylococcus Aureus Domain And A Fab Fragment Of A Human Igm Antibody
>gi|9246437|gb|AAF86053.1|AF210139_1 fntA-like protein [Staphylococcus aureus]
>gi|9230553|gb|AAF85897.1|AF165314_2 putative protein histidine kinase ArlS [Staphylococcus aureus]
>gi|9230552|gb|AAF85896.1|AF165314_1 putative response regulator ArlR [Staphylococcus aureus]
>gi|9181843|gb|AAF85653.1| orfX [Staphylococcus aureus]
>gi|9181842|gb|AAF85652.1| orf1260 [Staphylococcus aureus]
>gi|9181841|gb|AAF85651.1|AF181950_8 transposase [Staphylococcus aureus]
>gi|9181840|gb|AAF85650.1|AF181950_7 alpha protein [Staphylococcus aureus]
>gi|9181839|gb|AAF85649.1|AF181950_6 beta protein [Staphylococcus aureus]
>gi|9181838|gb|AAF85648.1|AF181950_5 bleomycin resistance protein [Staphylococcus aureus]
>gi|9181837|gb|AAF85647.1|AF181950_4 kanamycin resistance protein [Staphylococcus aureus]
>gi|9181836|gb|AAF85646.1|AF181950_3 transposase [Staphylococcus aureus]
>gi|9181835|gb|AAF85645.1|AF181950_1 low affinity penicillin binding protein [Staphylococcus aureus]
>gi|3603441|gb|AAC35853.1| type b beta-lactamase [Staphylococcus aureus]
>gi|8928563|sp|P81177|AURE_STAAU ZINC METALLOPROTEINASE AUREOLYSIN PRECURSOR (STAPHYLOCOCCUS AUREUS NEUTRAL PROTEINASE)
>gi|9049372|dbj|BAA99412.1| exfoliative toxin C [Staphylococcus aureus]
>gi|2495148|sp|Q53727|PCRA_STAAU ATP-DEPENDENT DNA HELICASE PCRA
>gi|115038|sp|P00807|BLAC_STAAU BETA-LACTAMASE PRECURSOR (PENICILLINASE)
>gi|3724158|emb|CAA06500.1| lipoprotein [Staphylococcus aureus]
>gi|3724157|emb|CAA06499.1| ATP binding protein [Staphylococcus aureus]
>gi|3724156|emb|CAA06498.1| membrane protein [Staphylococcus aureus]
>gi|3724155|emb|CAA06497.1| membrane protein [Staphylococcus aureus]
>gi|8885990|gb|AAF80331.1| enterotoxin I [Staphylococcus aureus]
>gi|8648965|emb|CAB94853.1| Map-ND2C protein [Staphylococcus aureus]
>gi|8569359|pdb|1EWC|A Chain A, Crystal Structure Of Zn2+ Loaded Staphylococcal Enterotoxin H
>gi|8134803|sp|Q92EH3|UVRC_STAAU EXCINUCLEASE ABC SUBUNIT C
>gi|8134747|sp|Q9Z5C3|TPIS_STAAU TRIOSEPHOSPHATE ISOMERASE (TIM)
>gi|8134611|sp|Q9Z5C4|PGK_STAAU PHOSPHOGLYCERATE KINASE
>gi|8134576|sp|O86491|MURE_STAAU UDP-N-ACETYLMURAMOYLALANYL-D-GLUTAMATE--2,6-DIAMINOPIMELATE LIGASE (UDP-N-ACETYLMURAMYL-TRIPLEPTIDE SYNTHETASE) (MESO-DIAMINOPIMELATE-ADDING ENZYME) (UDP-MURNAC-TRIPLEPTIDE SYNTHETASE)
>gi|7674177|sp|Q9ZAG8|RECU_STAAU RECOMBINATION PROTEIN U HOMOLOG (PENICILLIN-BINDING PROTEIN-RELATED FACTOR A HOMOLOG) (PBP RELATED FACTOR A HOMOLOG)
>gi|7674147|sp|Q9Z5C9|NRDI_STAAU NRDI PROTEIN
>gi|7388052|sp|O86490|RF3_STAAU PEPTIDE CHAIN RELEASE FACTOR 3 (RF-3)
>gi|7387927|sp|Q9ZEH5|MUS2_STAAU MUTS2 PROTEIN
>gi|7227940|sp|P95842|RSBV_STAAU ANTI-SIGMA B FACTOR ANTAGONIST
>gi|6920067|sp|P81683|EFG_STAAU ELONGATION FACTOR G (EF-G) (85 KDA VITRONECTIN BINDING PROTEIN)
>gi|6686369|sp|O32418|APT_STAAU ADENINE PHOSPHORIBOSYLTRANSFERASE (APRT)
>gi|6685442|sp|P56740|FOLB_STAAU DIHYDRONEOPTERIN ALDOLASE (DHNA)
>gi|6651452|gb|AAF22306.1|AF189239_1 repressor of toxins Rot [Staphylococcus aureus]
>gi|6647733|sp|O32419|RELA_STAAU GTP PYROPHOSPHOKINASE (ATP:GTP 3'-PYROPHOSPHOTRANSFERASE) (PPGPP SYNTHETASE I) ((P)PPGPP SYNTHETASE)
>gi|6647411|sp|Q9ZAH5|ALR_STAAU ALANINE RACEMASE
>gi|6226944|sp|O07322|MRAY_STAAU PHOSPHO-N-ACETYLMURAMOYL-PENTAPEPTIDE-TRANSFERASE (UDP-MURNAC-PENTAPEPTIDE PHOSPHOTRANSFERASE)
>gi|6226498|sp|O05337|YSI3_STAAU HYPOTHETICAL 30.4 KDA PROTEIN IN SIGMA70 OPERON (ORF30)
>gi|6225004|sp|Q9ZAH6|ACPS_STAAU HOLO-[ACYL-CARRIER PROTEIN] SYNTHASE (HOLO-ACP SYNTHASE)
>gi|3913884|sp|Q59801|HYSA_STAAU HYALURONATE LYASE PRECURSOR (HYALURONIDASE) (HYASE)
>gi|3122409|sp|O33595|MURD_STAAU UDP-N-ACETYLMURAMOYLALANINE--D-GLUTAMATE LIGASE (UDP-N-ACETYLMURAMOYL-L-ALANYL-D-GLUTAMATE SYNTHETASE) (D-GLUTAMIC ACID ADDING ENZYME)
>gi|3122408|sp|O31211|MURC_STAAU UDP-N-ACETYLMURAMATE--ALANINE LIGASE (UDP-N-ACETYLMURAMOYL-L-ALANINE SYNTHETASE)
>gi|2500720|sp|O06446|SECA_STAAU PREPROTEIN TRANSLOCASE SECA SUBUNIT
>gi|2499415|sp|Q59821|ODP2_STAAU DIHYDROLIPOAMIDE ACETYLTRANSFERASE COMPONENT OF PYRUVATE DEHYDROGENASE COMPLEX (E2)
>gi|2498749|sp|Q53726|PCRB_STAAU PCRB PROTEIN
>gi|2494749|sp|Q59812|GLNA_STAAU GLUTAMINE SYNTHETASE (GLUTAMATE--AMMONIA LIGASE) (GS)
>gi|2492949|sp|Q59803|AROC_STAAU CHORISMATE SYNTHASE (5-ENOLPYRUVYLSHIKIMATE-3-PHOSPHATE PHOSPHOLYASE)
>gi|1723227|sp|P52080|YAT3_STAAU HYPOTHETICAL 16.6 KDA PROTEIN IN ATL 5'REGION (ORF3)
>gi|1723225|sp|P52079|YAT2_STAAU HYPOTHETICAL 18.3 KDA PROTEIN IN ATL 5'REGION (ORF2)
>gi|1723223|sp|P52078|YAT1_STAAU HYPOTHETICAL PROTEIN IN ATL 5'REGION (ORF1)
>gi|1709887|sp|P51183|PT1_STAAU PHOSPHOENOLPYRUVATE-PROTEIN PHOSPHOTRANSFERASE (PHOSPHOTRANSFERASE SYSTEM, ENZYME I)
>gi|1708172|sp|P50915|HEM2_STAAU DELTA-AMINOLEVULINIC ACID DEHYDRATASE (PORPHOBILINOGEN SYNTHASE) (ALAD) (ALADH)

>gi|1174521|sp|P41972|SYI_STAAU ISOLEUCYL-TRNA SYNTHETASE (ISOLEUCINE--TRNA LIGASE) (ILERS)
>gi|1172890|sp|Q02350|RECA_STAAU RECA PROTEIN
>gi|1170027|sp|P45553|GRPE_STAAU GRPE PROTEIN (HSP-70 COFACTOR) (HSP20)
>gi|729030|sp|P39862|CAPM_STAAU CAPM PROTEIN
>gi|729026|sp|P39858|CAPI_STAAU CAPI PROTEIN
>gi|586026|sp|P02976|SPA1_STAAU IMMUNOGLOBULIN G BINDING PROTEIN A PRECURSOR (IGG BINDING PROTEIN A)
>gi|584922|sp|Q08854|CH60_STAAU 60 KDA CHAPERONIN (PROTEIN CPN60) (GROEL PROTEIN) (HEAT SHOCK PROTEIN 60)
>gi|461535|sp|Q05615|AROA_STAAU 3-PHOSPHOSHIKIMATE 1-CARBOXYVINYLTRANSFERASE (5-ENOLPYRUVYLSHIKIMATE-3-PHOSPHATE SYNTHASE) (EPSP SYNTHASE) (EPSPS)
>gi|400202|sp|P31024|LSPA_STAAU LIPOPROTEIN SIGNAL PEPTIDASE (PROLIPOPROTEIN SIGNAL PEPTIDASE) (SIGNAL PEPTIDASE II) (SPASE II)
>gi|141181|sp|P03861|YPL4_STAAU HYPOTHETICAL 14.6 KDA PROTEIN (READING FRAME C) (REPLICATION)
>gi|136616|sp|P13954|TYSY_STAAU THYMIDYLATE SYNTHASE (TS) (TSASE)
>gi|127193|sp|P02979|ERM2_STAAU RRNA ADENINE N-6-METHYLTRANSFERASE (MACROLIDE-LINCOSAMIDE-STREPTOGRAMIN B RESISTANCE PROTEIN) (ERYTHROMYCIN RESISTANCE PROTEIN)
>gi|125925|sp|P11100|LACD_STAAU TAGATOSE 1,6-DIPHOSPHATE ALDOLASE (TAGATOSE-BISPHOSPHATE ALDOLASE) (D-TAGATOSE-1,6-BISPHOSPHATE ALDOLASE)
>gi|125922|sp|P11099|LACC_STAAU TAGATOSE-6-PHOSPHATE KINASE (PHOSPHOTAGATOKINASE)
>gi|125919|sp|P26592|LACB_STAAU GALACTOSE-6-PHOSPHATE ISOMERASE LACB SUBUNIT
>gi|123185|sp|P01506|HLD_STAAU DELTA-HEMOLYSIN PRECURSOR (DELTA-TOXIN)
>gi|120457|sp|P14738|FNBA_STAAU FIBRONECTIN-BINDING PROTEIN PRECURSOR (FNBP)
>gi|113525|sp|P21545|AGRB_STAAU ACCESSORY GENE REGULATOR PROTEIN B
>gi|8101860|gb|AAAF72664.1|AF259960_1 major cold shock protein CspA [Staphylococcus aureus]
>gi|8099634|gb|AAAF72185.1|AF255950_1 AgrD signal peptide precursor [Staphylococcus aureus]
>gi|7959131|dbj|BAA95959.1| secretory protein SAI-B [Staphylococcus aureus]
>gi|7670327|dbj|BAA95014.1| TagG homolog [Staphylococcus aureus]
>gi|7670326|dbj|BAA95013.1| TagH homolog [Staphylococcus aureus]
>gi|7670325|dbj|BAA95012.1| TagA homolog [Staphylococcus aureus]
>gi|7670324|dbj|BAA95011.1| staphylokinase [Staphylococcus aureus]
>gi|7670323|dbj|BAA95010.1| hypothetical protein [Staphylococcus aureus]
>gi|7670322|dbj|BAA95009.1| KdpC homolog [Staphylococcus aureus]
>gi|7670321|dbj|BAA95008.1| KdpB homolog [Staphylococcus aureus]
>gi|7670320|dbj|BAA95007.1| KdpA homolog [Staphylococcus aureus]
>gi|7839534|gb|AAAF70313.1|AF260326_2 SrrB [Staphylococcus aureus]
>gi|7839533|gb|AAAF70312.1|AF260326_1 SrrA [Staphylococcus aureus]
>gi|7767013|pdb|1ENF|A Chain A, Crystal Structure Of Staphylococcal Enterotoxin H Determined To 1.69 A Resolution
>gi|3401995|pdb|2SPZ|A Chain A, Staphylococcal Protein A, Z-Domain, Nmr, 10 Structures
>gi|1280354|gb|AAA98144.1| ORFA [Staphylococcus aureus]
>gi|7594777|dbj|BAA82240.2| ORF CN050 [Staphylococcus aureus]
>gi|7594776|dbj|BAA82239.2| ORF CN049 [Staphylococcus aureus]
>gi|7594775|dbj|BAA82233.2| ORF N065 [Staphylococcus aureus]
>gi|7594774|dbj|BAA82227.2| ORF CN041 [Staphylococcus aureus]
>gi|7594773|dbj|BAA82226.2| ORF CN040 [Staphylococcus aureus]
>gi|7594772|dbj|BAA82223.2| ORF N060 [Staphylococcus aureus]
>gi|7594771|dbj|BAA82222.2| ORF CN038 [Staphylococcus aureus]
>gi|7594770|dbj|BAA94664.1| ORF N057 [Staphylococcus aureus]
>gi|7594769|dbj|BAA82219.2| methicillin resistance protein MecR1 [Staphylococcus aureus]
>gi|7594768|dbj|BAA82208.2| ORF N051 [Staphylococcus aureus]
>gi|7594767|dbj|BAA82207.2| ORF N050 [Staphylococcus aureus]
>gi|7594766|dbj|BAA82206.2| ORF N049 [Staphylococcus aureus]
>gi|7594765|dbj|BAA94663.1| ORF N043 [Staphylococcus aureus]
>gi|7594764|dbj|BAA94662.1| ORF N042 [Staphylococcus aureus]
>gi|7594763|dbj|BAA94661.1| ORF N041 [Staphylococcus aureus]
>gi|7594762|dbj|BAA94660.1| ORF N039 [Staphylococcus aureus]
>gi|7594761|dbj|BAA94659.1| ORF N038 [Staphylococcus aureus]
>gi|7594760|dbj|BAA94658.1| ORF N033 [Staphylococcus aureus]
>gi|7594759|dbj|BAA94657.1| ORF N032 [Staphylococcus aureus]
>gi|7594758|dbj|BAA94656.1| ORF N031 [Staphylococcus aureus]
>gi|7594757|dbj|BAA94655.1| ORF N030 [Staphylococcus aureus]
>gi|7594756|dbj|BAA94654.1| ORF N029 [Staphylococcus aureus]
>gi|7594755|dbj|BAA82191.2| ORF CN018 [Staphylococcus aureus]
>gi|7594754|dbj|BAA94653.1| ORF N024 [Staphylococcus aureus]
>gi|7594753|dbj|BAA82189.2| ORF CN017 [Staphylococcus aureus]
>gi|7594752|dbj|BAA82178.2| ORF CN007 [Staphylococcus aureus]
>gi|7594751|dbj|BAA94652.1| ORF N010 [Staphylococcus aureus]
>gi|7594750|dbj|BAA94651.1| ORF N009 [Staphylococcus aureus]
>gi|7594749|dbj|BAA94650.1| ORF N008 [Staphylococcus aureus]
>gi|7594748|dbj|BAA94649.1| ORF N007 [Staphylococcus aureus]
>gi|7594747|dbj|BAA82176.2| ORF CN005 [Staphylococcus aureus]

>gi|7594746|dbj|BAA94648.1| ORF N004 [Staphylococcus aureus]
 >gi|7594745|dbj|BAA94647.1| ORF CN004 [Staphylococcus aureus]
 >gi|7594744|dbj|BAA82175.2| ORF CN003 [Staphylococcus aureus]
 >gi|7594743|dbj|BAA82173.2| ORF CN002 [Staphylococcus aureus]
 >gi|7594742|dbj|BAA82171.2| ORF CN001 [Staphylococcus aureus]
 >gi|7592634|dbj|BAA94340.1| hypothetical protein [Staphylococcus aureus]
 >gi|7592633|dbj|BAA94339.1| hypothetical protein [Staphylococcus aureus]
 >gi|7592632|dbj|BAA94338.1| hypothetical protein [Staphylococcus aureus]
 >gi|7592631|dbj|BAA94337.1| hypothetical protein [Staphylococcus aureus]
 >gi|7592630|dbj|BAA94336.1| hypothetical protein [Staphylococcus aureus]
 >gi|7592629|dbj|BAA94335.1| hypothetical protein [Staphylococcus aureus]
 >gi|7592628|dbj|BAA94334.1| hypothetical protein [Staphylococcus aureus]
 >gi|7592627|dbj|BAA94333.1| hypothetical protein [Staphylococcus aureus]
 >gi|7592626|dbj|BAA94332.1| hypothetical protein [Staphylococcus aureus]
 >gi|7592625|dbj|BAA94331.1| hypothetical protein [Staphylococcus aureus]
 >gi|7592624|dbj|BAA94330.1| hypothetical protein [Staphylococcus aureus]
 >gi|7592623|dbj|BAA94329.1| hypothetical protein [Staphylococcus aureus]
 >gi|7592622|dbj|BAA94328.1| hypothetical protein [Staphylococcus aureus]
 >gi|7592621|dbj|BAA94327.1| hypothetical protein [Staphylococcus aureus]
 >gi|7592620|dbj|BAA94326.1| hypothetical protein [Staphylococcus aureus]
 >gi|7592619|dbj|BAA94325.1| hypothetical protein [Staphylococcus aureus]
 >gi|7592618|dbj|BAA86646.3| hypothetical protein [Staphylococcus aureus]
 >gi|7592617|dbj|BAA94324.1| hypothetical protein [Staphylococcus aureus]
 >gi|7592616|dbj|BAA94323.1| hypothetical protein [Staphylococcus aureus]
 >gi|7592615|dbj|BAA94322.1| hypothetical protein [Staphylococcus aureus]
 >gi|7592614|dbj|BAA86640.2| hypothetical protein [Staphylococcus aureus]
 >gi|7592613|dbj|BAA94321.1| hypothetical protein [Staphylococcus aureus]
 >gi|7592612|dbj|BAA94320.1| hypothetical protein [Staphylococcus aureus]
 >gi|7592611|dbj|BAA94319.1| hypothetical protein [Staphylococcus aureus]
 >gi|7592610|dbj|BAA94318.1| hypothetical protein [Staphylococcus aureus]
 >gi|7592609|dbj|BAA94317.1| hypothetical protein [Staphylococcus aureus]
 >gi|7592608|dbj|BAA94316.1| hypothetical protein [Staphylococcus aureus]
 >gi|7592607|dbj|BAA94315.1| hypothetical protein [Staphylococcus aureus]
 >gi|7592606|dbj|BAA94314.1| hypothetical protein [Staphylococcus aureus]
 >gi|6332771|dbj|BAA86653.1| open reading frame X [Staphylococcus aureus]
 >gi|6332770|dbj|BAA86652.1| transposase [Staphylococcus aureus]
 >gi|6332769|dbj|BAA86651.1| glycerophosphoryl diester phosphodiesterase homologue [Staphylococcus aureus]
 >gi|6332768|dbj|BAA86650.1| penicillin-binding protein 2' [Staphylococcus aureus]
 >gi|6332767|dbj|BAA86649.1| hypothetical protein [Staphylococcus aureus]
 >gi|6332766|dbj|BAA86648.1| cassette chromosome recombinase A1 [Staphylococcus aureus]
 >gi|6332765|dbj|BAA86647.1| hypothetical protein [Staphylococcus aureus]
 >gi|6332763|dbj|BAA86645.1| hypothetical protein [Staphylococcus aureus]
 >gi|6332762|dbj|BAA86644.1| hypothetical protein [Staphylococcus aureus]
 >gi|6332759|dbj|BAA86641.1| hypothetical protein [Staphylococcus aureus]
 >gi|6332757|dbj|BAA86639.1| hypothetical protein [Staphylococcus aureus]
 >gi|6332756|dbj|BAA86638.1| hypothetical protein [Staphylococcus aureus]
 >gi|6332755|dbj|BAA86637.1| hypothetical protein [Staphylococcus aureus]
 >gi|6332754|dbj|BAA86636.1| hypothetical protein [Staphylococcus aureus]
 >gi|6332753|dbj|BAA86635.1| hypothetical protein [Staphylococcus aureus]
 >gi|6332752|dbj|BAA86634.1| hypothetical protein [Staphylococcus aureus]
 >gi|6332751|dbj|BAA86633.1| hypothetical protein [Staphylococcus aureus]
 >gi|6332750|dbj|BAA86632.1| hypothetical protein [Staphylococcus aureus]
 >gi|5360873|dbj|BAA82243.1| orfX [Staphylococcus aureus]
 >gi|5360868|dbj|BAA82238.1| transposase for insertion sequence-like element IS431mec [Staphylococcus aureus]
 >gi|5360864|dbj|BAA82234.1| plasmid recombination enzyme [Staphylococcus aureus]
 >gi|5360860|dbj|BAA82230.1| bleomycin resistance protein(BRP) [Staphylococcus aureus]
 >gi|5360859|dbj|BAA82229.1| kanamycin nucleotidyltransferase [Staphylococcus aureus]
 >gi|5360858|dbj|BAA82228.1| transposase for insertion sequence-like element IS431mec [Staphylococcus aureus]
 >gi|5360854|dbj|BAA82224.1| glycerophosphoryldiester phosphodiesterase [Staphylococcus aureus]
 >gi|5360851|dbj|BAA82221.1| ORF N059 [Staphylococcus aureus]
 >gi|5360850|dbj|BAA82220.1| penicillin binding protein 2' [Staphylococcus aureus]
 >gi|5360848|dbj|BAA82218.1| methicillin resistance protein MecI [Staphylococcus aureus]
 >gi|5360847|dbj|BAA82217.1| ORF CN035 [Staphylococcus aureus]
 >gi|5360842|dbj|BAA82212.1| ORF CN032 [Staphylococcus aureus]
 >gi|5360841|dbj|BAA82211.1| ORF N052 [Staphylococcus aureus]
 >gi|5360840|dbj|BAA82210.1| ORF CN031 [Staphylococcus aureus]
 >gi|5360839|dbj|BAA82209.1| ORF CN030 [Staphylococcus aureus]
 >gi|5360835|dbj|BAA82205.1| rRNA adenine N-6-methyltransferase [Staphylococcus aureus]


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>gi|1361348|pir||H36891 transfer complex protein TrsG - Staphylococcus aureus
>gi|1361347|pir||G36891 transfer complex protein TrsF - Staphylococcus aureus
>gi|1361346|pir||F36891 transfer complex protein TrsE - Staphylococcus aureus
>gi|1361345|pir||E36891 transfer complex protein TrsD - Staphylococcus aureus
>gi|1361344|pir||D36891 transfer complex protein TrsC - Staphylococcus aureus
>gi|1361343|pir||C36891 transfer complex protein TrsB - Staphylococcus aureus
>gi|1361342|pir||B36891 transfer complex protein TrsA - Staphylococcus aureus
>gi|1361341|pir||S58708 neutral phosphatase - Staphylococcus aureus (ATCC 25923) (fragment)
>gi|1361340|pir||A55856 l1m protein - Staphylococcus aureus
>gi|1085937|pir||S42241 hypothetical protein 5 - Staphylococcus aureus plasmid pNS1
>gi|1085933|pir||S42240 hypothetical protein 4 - Staphylococcus aureus plasmid pNS1
>gi|1085928|pir||S42239 hypothetical protein 3 - Staphylococcus aureus plasmid pNS1
>gi|1085919|pir||S42237 hypothetical protein 2 - Staphylococcus aureus plasmid pNS1
>gi|1084189|pir||S54709 hypothetical protein 81 - Staphylococcus aureus
>gi|1075673|pir||S49271 hlgA-like protein precursor - Staphylococcus aureus
>gi|1075672|pir||S52267 DNA polymerase III - Staphylococcus aureus
>gi|1075671|pir||B55548 crtN protein - Staphylococcus aureus
>gi|1075670|pir||A55548 crtM protein - Staphylococcus aureus
>gi|1075668|pir||J2527 alkaline shock protein - Staphylococcus aureus
>gi|628922|pir||S43693 penicillin-binding protein 2 - Staphylococcus aureus
>gi|543692|pir||S42238 tetracyclin resistance protein - Staphylococcus aureus plasmid pNS1
>gi|541341|pir||S42926 hypothetical membrane spanning protein - Staphylococcus aureus
>gi|541340|pir||S42925 probable transport protein - Staphylococcus aureus
>gi|541339|pir||S39922 pcrB protein - Staphylococcus aureus
>gi|541336|pir||S41539 fibrinogen-binding protein - Staphylococcus aureus
>gi|541335|pir||A48620 adhesin - Staphylococcus aureus (fragment)
>gi|538880|pir||B24362 chloramphenicol O-acetyltransferase leader peptide - Staphylococcus aureus
plasmid pUB112
>gi|484391|pir||JN0627 leukocidin chain F precursor - Staphylococcus aureus
>gi|484390|pir||JN0626 leukocidin chain S precursor - Staphylococcus aureus
>gi|484389|pir||JN0625 gamma-hemolysin chain II precursor - Staphylococcus aureus
>gi|482713|pir||A61069 replication protein REP - Staphylococcus aureus plasmid pOX1000
>gi|482669|pir||A60998 replication protein REP - Staphylococcus aureus plasmid pOX2000
>gi|481955|pir||S40262 hypothetical protein C - Staphylococcus aureus
>gi|481954|pir||S40261 hypothetical protein B - Staphylococcus aureus
>gi|479952|pir||S35697 leukocidin chain F - Staphylococcus aureus
>gi|478296|pir||JN0822 acetyltransferase (EC 2.3.1.-) - Staphylococcus aureus
>gi|478043|pir||C49238 gamma-hemolysin component, HlgC - Staphylococcus aureus
>gi|477912|pir||B49238 gamma-hemolysin gamma 2 component, HlgB - Staphylococcus aureus
>gi|477911|pir||B49234 leucocidin R, component F - Staphylococcus aureus
>gi|477585|pir||A49234 leucocidin R S component - Staphylococcus aureus
>gi|421397|pir||S11782 regulatory protein blaI - Staphylococcus aureus plasmids
>gi|421395|pir||S11780 probable transposase - Staphylococcus aureus transposon Tn552
>gi|421394|pir||S11781 DNA-invertase - Staphylococcus aureus transposon Tn552
>gi|421393|pir||S11779 probable ATP-binding protein - Staphylococcus aureus transposon Tn552
>gi|421390|pir||JN0601 heat shock protein 60 - Staphylococcus aureus
>gi|421389|pir||JN0600 heat shock protein 10 - Staphylococcus aureus
>gi|421388|pir||S32419 gamma-hemolysin chain H gamma II - Staphylococcus aureus
>gi|421387|pir||S34270 fibrinogen-binding protein - Staphylococcus aureus
>gi|421386|pir||S34269 fibrinogen-binding protein - Staphylococcus aureus
>gi|421383|pir||S34444 blaZ protein - Staphylococcus aureus plasmid pI258 (fragment)
>gi|421379|pir||S34447 binR protein - Staphylococcus aureus plasmid pI258 (fragment)
>gi|322083|pir||S32211 leucocidin chain S - Staphylococcus aureus
>gi|322082|pir||S32212 leucocidin chain F - Staphylococcus aureus
>gi|320485|pir||A60633 tetracycline resistance protein - Staphylococcus aureus (strain MRSA101)
>gi|320484|pir||A37389 repN protein - Staphylococcus aureus plasmid pCW7
>gi|320483|pir||C60634 probable transposase - Staphylococcus aureus insertion sequence IS257-3
>gi|320482|pir||B60634 probable transposase - Staphylococcus aureus insertion sequence IS257-2
>gi|320481|pir||A60634 probable transposase - Staphylococcus aureus insertion sequence IS257-1
>gi|320480|pir||A60757 enterotoxin C-1 - Staphylococcus aureus (fragments)
>gi|282254|pir||A41903 recombinase homolog - Staphylococcus aureus (fragment)
>gi|282253|pir||F42721 recombination protein recA - Staphylococcus aureus (fragment)
>gi|282251|pir||S28101 hypothetical protein 2 - Staphylococcus aureus plasmid pC223
>gi|282250|pir||S28102 rlx protein - Staphylococcus aureus plasmid pC223
>gi|282249|pir||S26352 hypothetical protein - Staphylococcus aureus transposon Tn4001
>gi|282243|pir||A42404 collagen adhesin - Staphylococcus aureus
>gi|282241|pir||E41903 recombinase Bin3 - Staphylococcus aureus (fragment)
>gi|282237|pir||S26353 aminoglycoside resistance protein aacA-aphD - Staphylococcus aureus
transposon Tn4001
>gi|282236|pir||A43848 cell surface adhesin for heparan sulfate, 66K - Staphylococcus aureus
(fragment)

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>gi|282235|pir||B43848 cell surface adhesin for heparan sulfate, 60K - *Staphylococcus aureus* (fragment)
>gi|280218|pir||A60450 hypothetical protein att155 - *Staphylococcus aureus* (fragment)
>gi|280217|pir||A44506 lactose operon repressor lacR - *Staphylococcus aureus*
>gi|97855|pir||JC1204 vga protein - *Staphylococcus aureus*
>gi|97854|pir||S12706 type II site-specific deoxyribonuclease (EC 3.1.21.4) Sau96I - *Staphylococcus aureus*
>gi|97850|pir||A41511 staphylocoagulase precursor - *Staphylococcus aureus* (strain BB)
>gi|97847|pir||JQ0759 restriction endonuclease (EC 3.1.-.-) - *Staphylococcus aureus*
>gi|97846|pir||S09566 repB protein - *Staphylococcus aureus* plasmid pBD64
>gi|97844|pir||B36242 quinolone resistance protein norA8736 - *Staphylococcus aureus* plasmid pMR8736 (fragment)
>gi|97843|pir||S12394 probable transport protein qacA - *Staphylococcus aureus* plasmid pSK1
>gi|97838|pir||S12093 probable transposase - *Staphylococcus aureus* insertion sequence IS431mec
>gi|97836|pir||A36242 norA209 protein - *Staphylococcus aureus* plasmid pSA209 (fragment)
>gi|97835|pir||A37838 norA protein - *Staphylococcus aureus*
>gi|97834|pir||S09565 neomycin resistance protein - *Staphylococcus aureus* plasmid pBD64
>gi|97831|pir||JQ0773 penicillin-binding protein mecA, low-affinity - *Staphylococcus aureus*
>gi|97830|pir||S19207 leucocidin R component F precursor - *Staphylococcus aureus*
>gi|97829|pir||A30471 hypothetical protein rep - *Staphylococcus aureus* plasmid pSK89
>gi|97828|pir||B30471 hypothetical protein cop - *Staphylococcus aureus* plasmid pSK89
>gi|97824|pir||S20793 hypothetical protein 5 - *Staphylococcus aureus*
>gi|97820|pir||S12393 hypothetical protein (qacA 5' region) - *Staphylococcus aureus* plasmid pSK1
>gi|97819|pir||S14179 hypothetical protein 140 - *Staphylococcus aureus*
>gi|97815|pir||B38158 galactose-6-phosphate isomerase 19K chain - *Staphylococcus aureus*
>gi|97814|pir||A38158 galactose-6-phosphate isomerase (EC 5.1.3.-) 15K chain - *Staphylococcus aureus*
>gi|97813|pir||S19702 fibronectin-binding protein B - *Staphylococcus aureus*
>gi|97812|pir||A32192 fibronectin-binding protein - *Staphylococcus aureus*
>gi|97804|pir||S16509 DNA-invertase - *Staphylococcus aureus* transposon Tn552
>gi|97795|pir||S09246 coagulase precursor - *Staphylococcus aureus* (strain 8325-4)
>gi|97793|pir||C34643 cathepsin E (EC 3.4.23.34) - *Staphylococcus aureus* (fragments)
>gi|97788|pir||S09385 DNA-invertase homolog bin3 - *Staphylococcus aureus* transposon Tn555
>gi|97786|pir||S15324 beta-hemolysin - *Staphylococcus aureus*
>gi|97783|pir||B41589 40K elastin-binding protein - *Staphylococcus aureus* (fragment)
>gi|97782|pir||A41589 25K elastin-binding protein - *Staphylococcus aureus* (fragment)
>gi|80324|pir||A24456 kanamycin nucleotidyltransferase (EC 2.7.7.-) - *Staphylococcus aureus* plasmid pUB110
>gi|79917|pir||S06782 tryptophan synthase (EC 4.2.1.20) - *Staphylococcus aureus* (fragment)
>gi|79916|pir||A24545 triacylglycerol lipase (EC 3.1.1.3) - *Staphylococcus aureus*
>gi|79915|pir||C24584 transposition regulatory protein tnpC - *Staphylococcus aureus* transposon Tn554
>gi|79914|pir||B24584 transposition regulatory protein tnpB - *Staphylococcus aureus* transposon Tn554
>gi|79913|pir||A24584 transposition regulatory protein tnpA - *Staphylococcus aureus* transposon Tn554
>gi|79912|pir||S04166 transposase 2 - *Staphylococcus aureus* transposon Tn4003
>gi|79911|pir||S04162 transposase 1 - *Staphylococcus aureus* transposon Tn4003
>gi|79910|pir||JS0296 transposase - *Staphylococcus aureus*
>gi|79906|pir||S06744 staphylocoagulase precursor - *Staphylococcus aureus*
>gi|79905|pir||A25620 staphylocoagulase - *Staphylococcus aureus* (fragment)
>gi|79903|pir||S00935 rlx protein - *Staphylococcus aureus* plasmid pS194
>gi|79902|pir||A29827 replication protein REP - *Staphylococcus aureus* plasmids
>gi|79901|pir||S00909 replication initiation protein - *Staphylococcus aureus* plasmid pC223
>gi|79900|pir||A30480 repJ protein - *Staphylococcus aureus* plasmid pC223
>gi|79899|pir||JT0372 repI protein - *Staphylococcus aureus* plasmid pUB112
>gi|79898|pir||S00937 repE protein - *Staphylococcus aureus* plasmid pS194
>gi|79896|pir||A29605 protein A precursor - *Staphylococcus aureus* (strain Cowan 1)
>gi|79894|pir||S20576 probable regulatory protein mecI - *Staphylococcus aureus*
>gi|79891|pir||B28474 phosphotransferase system enzyme II (EC 2.7.1.69), lactose-specific, factor II - *Staphylococcus aureus*
>gi|79887|pir||JQ1147 N-acetylmuramoyl-L-alanine amidase (EC 3.5.1.28) - *Staphylococcus aureus*
>gi|79886|pir||JQ1439 multidrug resistance protein - *Staphylococcus aureus* plasmids
>gi|79884|pir||G29504 hypothetical 20K protein (mer regulatory region) - *Staphylococcus aureus* plasmid pI258
>gi|79883|pir||C29504 hypothetical 24K protein (mer operon) - *Staphylococcus aureus* plasmid pI258
>gi|79882|pir||B29504 hypothetical 18K protein (mer operon) - *Staphylococcus aureus* plasmid pI258
>gi|79881|pir||A29504 hypothetical 16K protein (mer operon) - *Staphylococcus aureus* plasmid pI258
>gi|79880|pir||D29504 hypothetical 14K protein (mer operon) - *Staphylococcus aureus* plasmid pI258
>gi|79879|pir||S20575 mecR1 protein - *Staphylococcus aureus*
>gi|79877|pir||A31901 lincomycin resistance protein linA' - *Staphylococcus aureus* (strain BM4611)
>gi|79875|pir||JQ1530 leukocidin chain F precursor - *Staphylococcus aureus*
>gi|79874|pir||S04359 lacD protein - *Staphylococcus aureus*
>gi|79871|pir||S00936 hypothetical protein D - *Staphylococcus aureus* plasmid pS194
>gi|79869|pir||S15767 hypothetical protein 2 (h1b 3' region) - *Staphylococcus aureus* (fragment)

>gi|79868|pir||S15765 hypothetical protein 1 (h1b 5' region) - Staphylococcus aureus (fragment)
 >gi|79867|pir||F24584 hypothetical protein - Staphylococcus aureus transposon Tn554
 >gi|79866|pir||S04165 hypothetical protein - Staphylococcus aureus plasmid pSK1 transposon Tn4003
 >gi|79865|pir||S06784 hypothetical protein (femA 3' region) - Staphylococcus aureus
 >gi|79864|pir||B32561 cadC protein - Staphylococcus aureus plasmid pI258
 >gi|79863|pir||A41652 probable glycerophosphodiester phosphodiesterase (EC 3.1.4.46) - Staphylococcus aureus
 >gi|79862|pir||S06783 femA protein - Staphylococcus aureus
 >gi|79857|pir||JG0016 epidermal cell differentiation inhibitor precursor - Staphylococcus aureus
 >gi|79843|pir||JQ0387 agrB protein - Staphylococcus aureus
 >gi|79842|pir||A32357 accessory gene regulatory protein agrA - Staphylococcus aureus
 >gi|7437965|pir||JC6560 UDP-N-acetylmuramoylalanine--D-glutamate ligase (EC 6.3.2.9) - Staphylococcus aureus
 >gi|7434769|pir||S34442 transcription initiation factor sigma plaC - Staphylococcus aureus
 >gi|2144945|pir||QVSAA protein A precursor - Staphylococcus aureus
 >gi|2144683|pir||ENSAC1 enterotoxin C-1 precursor - Staphylococcus aureus
 >gi|2144682|pir||ENSAB6 enterotoxin B precursor - Staphylococcus aureus
 >gi|2126578|pir||S54426 DNA topoisomerase (ATP-hydrolyzing) (EC 5.99.1.3) chain B - Staphylococcus aureus
 >gi|2126577|pir||S54427 gyrase-like protein alpha chain - Staphylococcus aureus
 >gi|2126576|pir||S59956 DNA-directed RNA polymerase (EC 2.7.7.6) beta' chain - Staphylococcus aureus (fragment)
 >gi|2119116|pir||S59954 ribosomal protein L7/L12 - Staphylococcus aureus (fragment)
 >gi|2117996|pir||A53641 arsenate reductase (EC 1.-.-.-) - Staphylococcus aureus plasmid pI258
 >gi|2117910|pir||S59951 DNA-directed RNA polymerase (EC 2.7.7.6) beta chain - Staphylococcus aureus
 >gi|1363411|pir||S58814 cell division protein ftsZ - Staphylococcus aureus
 >gi|1361350|pir||A56976 transfer complex protein TrsI - Staphylococcus aureus
 >gi|1084187|pir||S54708 DNA-directed DNA polymerase (EC 2.7.7.7) III beta chain - Staphylococcus aureus
 >gi|1075676|pir||S54793 superoxide dismutase (EC 1.15.1.1) (Fe/Mn) - Staphylococcus aureus (fragment)
 >gi|1075669|pir||S52934 alkyl hydroperoxide reductase (EC 1.6.4.-) c22 protein - Staphylococcus aureus (fragment)
 >gi|625852|pir||JP0045 ribosomal protein L30 - Staphylococcus aureus (fragment)
 >gi|541338|pir||S39923 DNA helicase pcrA - Staphylococcus aureus
 >gi|541337|pir||S40178 isoleucine--tRNA ligase (EC 6.1.1.5) - Staphylococcus aureus
 >gi|538884|pir||B46568 ermC protein - Staphylococcus aureus plasmid pT48
 >gi|538882|pir||A40585 DNA topoisomerase (ATP-hydrolyzing) (EC 5.99.1.3) chain B - Staphylococcus aureus
 >gi|538881|pir||B40585 DNA topoisomerase (ATP-hydrolyzing) (EC 5.99.1.3) chain A - Staphylococcus aureus
 >gi|538608|pir||A24362 chloramphenicol O-acetyltransferase (EC 2.3.1.28) - Staphylococcus aureus plasmid pUB112
 >gi|482777|pir||A61152 chloramphenicol O-acetyltransferase (EC 2.3.1.28) - Staphylococcus aureus plasmid pSCS7
 >gi|421382|pir||S11783 bla regulator protein blaR1 - Staphylococcus aureus plasmids
 >gi|322081|pir||S32014 dihydrofolate reductase (EC 1.5.1.3) - Staphylococcus aureus
 >gi|322080|pir||A44849 chloramphenicol O-acetyltransferase (EC 2.3.1.28) - Staphylococcus aureus plasmid
 >gi|282240|pir||B41903 arsenical resistance operon repressor - Staphylococcus aureus plasmid pI258
 >gi|282239|pir||D41903 arsenate reductase (EC 1.-.-.-) - Staphylococcus aureus plasmid pI258
 >gi|282238|pir||C41903 arsenical pump membrane protein - Staphylococcus aureus
 >gi|279459|pir||YXSAT3 thymidylate synthase (EC 2.1.1.45) - Staphylococcus aureus plasmid pSK1 transposon Tn4003
 >gi|98263|pir||A36141 cop protein - Staphylococcus aureus plasmid pE194
 >gi|97849|pir||S12705 site-specific DNA-methyltransferase (cytosine-specific) (EC 2.1.1.73) Sau96I - Staphylococcus aureus
 >gi|97842|pir||S19721 pyruvate dehydrogenase (lipoamide) (EC 1.2.4.1) chain E1-beta - Staphylococcus aureus (fragment)
 >gi|97837|pir||A31048 phosphotransferase system enzyme II (EC 2.7.1.69), mannitol-specific, factor III - Staphylococcus aureus (fragments)
 >gi|97833|pir||JQ0760 methyltransferase (EC 2.1.1.-) - Staphylococcus aureus
 >gi|97832|pir||S20433 lipoprotein signal peptidase (EC 3.4.23.36) - Staphylococcus aureus
 >gi|97826|pir||S20799 hypothetical protein 7 - Staphylococcus aureus
 >gi|97816|pir||S21758 glutamic acid-specific endopeptidase - Staphylococcus aureus
 >gi|97807|pir||A33953 enterotoxin D precursor - Staphylococcus aureus
 >gi|97805|pir||S11885 enterotoxin C3 - Staphylococcus aureus
 >gi|97798|pir||S19723 dihydrolipoamide dehydrogenase (EC 1.8.1.4) - Staphylococcus aureus
 >gi|97797|pir||S19722 dihydrolipoamide S-acetyltransferase (EC 2.3.1.12) chain E2 - Staphylococcus aureus
 >gi|97787|pir||A35001 beta-lactamase (EC 3.5.2.6) PSE-4 precursor - Staphylococcus aureus

>gi|80332|pir||B29827 macrolide/lincosamide/streptogramin B resistance methylase - Staphylococcus aureus plasmid pE5
 >gi|79907|pir||S00938 str protein - Staphylococcus aureus plasmid pS194
 >gi|79904|pir||D24584 spectinomycin resistance protein spc - Staphylococcus aureus transposon Tn554
 >gi|79893|pir||A32561 probable cadmium-transporting ATPase (EC 3.6.1.-) - Staphylococcus aureus
 >gi|79888|pir||F29504 alkylmercury lyase (EC 4.99.1.2) - Staphylococcus aureus plasmid pI258
 >gi|79885|pir||E29504 mercury(II) reductase (EC 1.16.1.1) - Staphylococcus aureus plasmid pI258
 >gi|79878|pir||A25101 erythromycin resistance protein ermA - Staphylococcus aureus transposon Tn554
 >gi|79873|pir||S04358 lacC protein - Staphylococcus aureus
 >gi|79861|pir||A26050 exfoliative toxin B precursor - Staphylococcus aureus
 >gi|79856|pir||A28179 enterotoxin E precursor - Staphylococcus aureus
 >gi|79855|pir||A60114 enterotoxin C-2 precursor - Staphylococcus aureus
 >gi|79853|pir||A28664 enterotoxin A precursor - Staphylococcus aureus
 >gi|79851|pir||S04164 dihydrofolate reductase (EC 1.5.1.3) - Staphylococcus aureus plasmid pSK1 transposon Tn4003
 >gi|79844|pir||A27233 beta-galactosidase (EC 3.2.1.23) - Staphylococcus aureus
 >gi|76321|pir||QQSAC2 hypothetical protein C - Staphylococcus aureus plasmid pC221
 >gi|76320|pir||QQSAA2 rlx protein - Staphylococcus aureus plasmid pC221
 >gi|76319|pir||QQSA8T hypothetical protein B-189 - Staphylococcus aureus plasmid pT181
 >gi|76318|pir||QQSAEC hypothetical protein E-229 - Staphylococcus aureus plasmid pC194
 >gi|76317|pir||QQSACC hypothetical protein C-120 - Staphylococcus aureus plasmid pC194
 >gi|76316|pir||QQSA7C hypothetical protein E-74 - Staphylococcus aureus plasmid pC194
 >gi|76315|pir||QQSACE hypothetical protein C-102 - Staphylococcus aureus plasmid pE194
 >gi|76314|pir||QQSABE hypothetical protein B-111 - Staphylococcus aureus plasmid pE194
 >gi|73155|pir||RQSAD2 repD protein - Staphylococcus aureus plasmid pC221
 >gi|73154|pir||RQSACT repC protein - Staphylococcus aureus plasmids
 >gi|73152|pir||LFSA9P ermC leader peptide - Staphylococcus aureus plasmids
 >gi|72984|pir||QQSA4E hypothetical protein C-403 - Staphylococcus aureus plasmid pE194
 >gi|72843|pir||QQSACT hypothetical protein C-156 - Staphylococcus aureus plasmid pT181
 >gi|72842|pir||QQSABT hypothetical protein B-295 - Staphylococcus aureus plasmid pT181
 >gi|72420|pir||WPSAHP phosphotransferase system phosphohistidine-containing protein - Staphylococcus aureus
 >gi|69625|pir||XCSAS1 toxic shock syndrome toxin-1 precursor - Staphylococcus aureus
 >gi|69556|pir||LESAD delta hemolysin - Staphylococcus aureus
 >gi|67766|pir||PNSAP beta-lactamase (EC 3.5.2.6) precursor - Staphylococcus aureus
 >gi|67543|pir||PRSAEB epidermolytic toxin B precursor - Staphylococcus aureus plasmid pRW001
 >gi|67542|pir||PRSAEA epidermolytic toxin A precursor - Staphylococcus aureus
 >gi|67541|pir||PRSASK glutamyl endopeptidase (EC 3.4.21.19) precursor - Staphylococcus aureus
 >gi|67305|pir||NCSAF micrococcal nuclease (EC 3.1.31.1) precursor - Staphylococcus aureus
 >gi|66882|pir||PKSAF kanamycin kinase (EC 2.7.1.95) - Staphylococcus aureus
 >gi|66872|pir||WQSA3L phosphotransferase system enzyme II (EC 2.7.1.69), lactose-specific, factor III - Staphylococcus aureus
 >gi|66524|pir||XXSAC2 chloramphenicol O-acetyltransferase (EC 2.3.1.28) - Staphylococcus aureus plasmid pC221
 >gi|66523|pir||XXSACC chloramphenicol O-acetyltransferase (EC 2.3.1.28) - Staphylococcus aureus plasmids
 >gi|66452|pir||YESA9E rRNA (adenine-N6-)-methyltransferase (EC 2.1.1.48) - Staphylococcus aureus plasmids
 >gi|7381167|gb|AAF61418.1|AF135268_1 ribonuclease P protein component [Staphylococcus aureus]
 >gi|6648971|gb|AAF21314.1| site-specific recombinase [Staphylococcus aureus]
 >gi|6648970|gb|AAF21313.1|AF118839_1 iron uptake regulatory protein; Fur [Staphylococcus aureus]
 >gi|7330783|gb|AAF60251.1| Geh [Staphylococcus aureus]
 >gi|7330782|gb|AAF60250.1| IcaC [Staphylococcus aureus]
 >gi|7330780|gb|AAF60249.1| Geh [Staphylococcus aureus]
 >gi|7330779|gb|AAF60248.1| IcaC [Staphylococcus aureus]
 >gi|7330777|gb|AAF60247.1| Geh [Staphylococcus aureus]
 >gi|7330776|gb|AAF60246.1| IcaC [Staphylococcus aureus]
 >gi|7330774|gb|AAF60245.1| Geh [Staphylococcus aureus]
 >gi|7330773|gb|AAF60244.1| IcaC [Staphylococcus aureus]
 >gi|7330771|gb|AAF60243.1| Geh [Staphylococcus aureus]
 >gi|7330770|gb|AAF60242.1| IcaC [Staphylococcus aureus]
 >gi|7330768|gb|AAF60241.1| HprK [Staphylococcus aureus]
 >gi|7330767|gb|AAF60240.1| UvrA [Staphylococcus aureus]
 >gi|7330765|gb|AAF60239.1| HprK [Staphylococcus aureus]
 >gi|7330764|gb|AAF60238.1| UvrA [Staphylococcus aureus]
 >gi|7330762|gb|AAF60237.1| HprK [Staphylococcus aureus]
 >gi|7330761|gb|AAF60236.1| UvrA [Staphylococcus aureus]
 >gi|7330759|gb|AAF60235.1| HprK [Staphylococcus aureus]
 >gi|7330758|gb|AAF60234.1| UvrA [Staphylococcus aureus]
 >gi|7330756|gb|AAF60233.1| HprK [Staphylococcus aureus]
 >gi|7330755|gb|AAF60232.1| UvrA [Staphylococcus aureus]

>gi|7330753|gb|AAF60231.1| HprK [Staphylococcus aureus]
 >gi|7330752|gb|AAF60230.1| UvrA [Staphylococcus aureus]
 >gi|6671351|gb|AAF23170.1|AF210055_3 AgrC [Staphylococcus aureus]
 >gi|6671350|gb|AAF23169.1|AF210055_2 AgrD [Staphylococcus aureus]
 >gi|6671349|gb|AAF23168.1|AF210055_1 AgrB [Staphylococcus aureus]
 >gi|7328298|emb|CAB82464.1| transketolase, putative [Staphylococcus aureus]
 >gi|7328297|emb|CAB82463.1| SOS regulatory LexA protein, putative [Staphylococcus aureus]
 >gi|7328295|emb|CAB82462.1| DNA mismatch repair protein [Staphylococcus aureus]
 >gi|7328294|emb|CAB82461.1| DNA mismatch repair protein [Staphylococcus aureus]
 >gi|7328292|emb|CAB82460.1| hypothetical protein [Staphylococcus aureus]
 >gi|7328291|emb|CAB82459.1| hypothetical protein [Staphylococcus aureus]
 >gi|7328290|emb|CAB82458.1| hypothetical protein [Staphylococcus aureus]
 >gi|7328289|emb|CAB82457.1| hypothetical protein [Staphylococcus aureus]
 >gi|7328288|emb|CAB82456.1| hypothetical protein [Staphylococcus aureus]
 >gi|7328284|emb|CAB82466.1| MutS protein [Staphylococcus aureus]
 >gi|7328280|emb|CAB82478.1| hypothetical protein [Staphylococcus aureus]
 >gi|7328279|emb|CAB82477.1| hypothetical protein [Staphylococcus aureus]
 >gi|7328278|emb|CAB82476.1| hypothetical protein [Staphylococcus aureus]
 >gi|7328277|emb|CAB82475.1| D-alanine aminotransferase [Staphylococcus aureus]
 >gi|7328276|emb|CAB82474.1| putative peptidase [Staphylococcus aureus]
 >gi|7328275|emb|CAB82473.1| hypothetical protein [Staphylococcus aureus]
 >gi|7328274|emb|CAB82472.1| hypothetical protein [Staphylococcus aureus]
 >gi|7328272|emb|CAB82471.1| ORF314 [Staphylococcus aureus]
 >gi|7328271|emb|CAB82470.1| hypothetical protein [Staphylococcus aureus]
 >gi|7328270|emb|CAB82469.1| hypothetical protein [Staphylococcus aureus]
 >gi|7328269|emb|CAB82468.1| hypothetical protein [Staphylococcus aureus]
 >gi|7106006|emb|CAB75986.1| ornithine carbamoyltransferase [Staphylococcus aureus]
 >gi|7272362|gb|AAA26601.2| blaZ [Staphylococcus aureus]
 >gi|152968|gb|AAA26604.1| binR [Staphylococcus aureus]
 >gi|152967|gb|AAA26603.1| blaI [Staphylococcus aureus]
 >gi|152966|gb|AAA26602.1| blaR1 [Staphylococcus aureus]
 >gi|7242216|gb|AAB32123.2| porphobilinogen synthase; PBG; HemB [Staphylococcus aureus]
 >gi|7239722|gb|AAA71951.2| putative [Staphylococcus aureus]
 >gi|7239370|gb|AAF43206.1|AF230358_3 accessory gene regulator protein D [Staphylococcus aureus]
 >gi|7239369|gb|AAF43205.1|AF230358_2 accessory gene regulator protein B [Staphylococcus aureus]
 >gi|7239368|gb|AAF43204.1|AF230358_1 delta-haemolysin precursor [Staphylococcus aureus]
 >gi|310620|gb|AAA71964.1| putative [Staphylococcus aureus]
 >gi|310619|gb|AAA71963.1| putative [Staphylococcus aureus]
 >gi|310618|gb|AAA71962.1| putative [Staphylococcus aureus]
 >gi|310617|gb|AAA71961.1| putative [Staphylococcus aureus]
 >gi|310616|gb|AAA71960.1| putative [Staphylococcus aureus]
 >gi|310615|gb|AAA71959.1| putative [Staphylococcus aureus]
 >gi|310614|gb|AAA71958.1| putative [Staphylococcus aureus]
 >gi|310613|gb|AAA71957.1| putative [Staphylococcus aureus]
 >gi|310612|gb|AAA71956.1| putative [Staphylococcus aureus]
 >gi|310611|gb|AAA71955.1| putative [Staphylococcus aureus]
 >gi|310610|gb|AAA71954.1| putative [Staphylococcus aureus]
 >gi|310609|gb|AAA71953.1| putative [Staphylococcus aureus]
 >gi|310608|gb|AAA71952.1| putative [Staphylococcus aureus]
 >gi|4126683|dbj|BAA36693.1| enterotoxin type Gv [Staphylococcus aureus]
 >gi|7162103|emb|CAB76672.1| phosphate actyltransferase [Staphylococcus aureus]
 >gi|7162101|emb|CAB76671.1| phosphate actyltransferase [Staphylococcus aureus]
 >gi|7162099|emb|CAB76670.1| phosphate actyltransferase [Staphylococcus aureus]
 >gi|7162097|emb|CAB76669.1| phosphate actyltransferase [Staphylococcus aureus]
 >gi|7162095|emb|CAB76668.1| phosphate actyltransferase [Staphylococcus aureus]
 >gi|7162093|emb|CAB76667.1| phosphate actyltransferase [Staphylococcus aureus]
 >gi|7162091|emb|CAB76666.1| phosphate actyltransferase [Staphylococcus aureus]
 >gi|7162089|emb|CAB76665.1| phosphate actyltransferase [Staphylococcus aureus]
 >gi|7162087|emb|CAB76664.1| phosphate actyltransferase [Staphylococcus aureus]
 >gi|7162085|emb|CAB76663.1| phosphate actyltransferase [Staphylococcus aureus]
 >gi|7162083|emb|CAB76662.1| phosphate actyltransferase [Staphylococcus aureus]
 >gi|7162081|emb|CAB76661.1| phosphate actyltransferase [Staphylococcus aureus]
 >gi|7162079|emb|CAB76660.1| phosphate actyltransferase [Staphylococcus aureus]
 >gi|7162077|emb|CAB76659.1| phosphate actyltransferase [Staphylococcus aureus]
 >gi|7162075|emb|CAB76658.1| phosphate actyltransferase [Staphylococcus aureus]
 >gi|7162073|emb|CAB76657.1| triosephosphate isomerase [Staphylococcus aureus]
 >gi|7162071|emb|CAB76656.1| triosephosphate isomerase [Staphylococcus aureus]
 >gi|7162069|emb|CAB76655.1| triosephosphate isomerase [Staphylococcus aureus]
 >gi|7162067|emb|CAB76654.1| triosephosphate isomerase [Staphylococcus aureus]
 >gi|7162065|emb|CAB76653.1| triosephosphate isomerase [Staphylococcus aureus]
 >gi|7162063|emb|CAB76652.1| triosephosphate isomerase [Staphylococcus aureus]

>gi|7161911|emb|CAB76580.1| acetyl coenzyme A acetyltransferase [Staphylococcus aureus]
>gi|7161909|emb|CAB76579.1| acetyl coenzyme A acetyltransferase [Staphylococcus aureus]
>gi|7161907|emb|CAB76578.1| acetyl coenzyme A acetyltransferase [Staphylococcus aureus]
>gi|7161905|emb|CAB76577.1| acetyl coenzyme A acetyltransferase [Staphylococcus aureus]
>gi|7161903|emb|CAB76576.1| acetyl coenzyme A acetyltransferase [Staphylococcus aureus]
>gi|7161901|emb|CAB76575.1| acetyl coenzyme A acetyltransferase [Staphylococcus aureus]
>gi|7161899|emb|CAB76574.1| acetyl coenzyme A acetyltransferase [Staphylococcus aureus]
>gi|7161897|emb|CAB76573.1| acetyl coenzyme A acetyltransferase [Staphylococcus aureus]
>gi|7161887|emb|CAB76839.1| Catalase [Staphylococcus aureus]
>gi|7161885|emb|CAB76840.1| Catalase [Staphylococcus aureus]
>gi|7107452|gb|AAF36410.1|AF235026_1 pyruvate dehydrogenase beta subunit PdhB [Staphylococcus aureus]
>gi|7106008|emb|CAB75987.1| ornithine carbamoyltransferase Otc6850 [Staphylococcus aureus]
>gi|7106004|emb|CAB75985.1| extracellular matrix and plasma binding protein [Staphylococcus aureus]
>gi|7106002|emb|CAB75984.1| extracellular matrix and plasma binding protein [Staphylococcus aureus]
>gi|7019229|emb|CAB75732.1| bone sialoprotein-binding protein [Staphylococcus aureus]
>gi|6180191|gb|AAF05840.1|AF197058_1 trans-2-enoyl-ACP reductase [Staphylococcus aureus]
>gi|6967305|emb|CAB72943.1| hypothetical protein [Staphylococcus aureus]
>gi|6967304|emb|CAB72942.1| hypothetical protein [Staphylococcus aureus]
>gi|6967303|emb|CAB72941.1| hypothetical protein [Staphylococcus aureus]
>gi|6967301|emb|CAB72940.1| hypothetical protein [Staphylococcus aureus]
>gi|6967300|emb|CAB72939.1| hypothetical protein [Staphylococcus aureus]
>gi|6912039|emb|CAB72261.1| penicillin-binding protein 3 [Staphylococcus aureus]
>gi|2506027|dbj|BAA22600.1| NAG [Staphylococcus aureus]
>gi|577649|dbj|BAA07715.1| preLUKM [Staphylococcus aureus]
>gi|216971|dbj|BAA00630.1| glutamic acid specific protease prepropeptide [Staphylococcus aureus]
>gi|6119707|emb|CAB59570.1| aureolysin [Staphylococcus aureus]
>gi|6119705|emb|CAB59569.1| aureolysin [Staphylococcus aureus]
>gi|6119703|emb|CAB59568.1| aureolysin [Staphylococcus aureus]
>gi|6119701|emb|CAB59567.1| aureolysin [Staphylococcus aureus]
>gi|6729657|emb|CAB67709.1| secretory protein [Staphylococcus aureus]
>gi|6729716|pdb|1BQB|A Chain A, Aureolysin, Staphylococcus Aureus Metalloproteinase
>gi|5107600|pdb|1KGG|A Chain A, Structure Of Beta-Lactamase Glu166Gln:asn170asp Mutant
>gi|6110605|gb|AAF03894.1|AF193842_1 DNA polymerase I [Staphylococcus aureus]
>gi|6690335|gb|AAF24091.1|AF117259_3 ATP binding protein VgA [Staphylococcus aureus]
>gi|6690334|gb|AAF24090.1|AF117259_2 unknown [Staphylococcus aureus]
>gi|6690333|gb|AAF24089.1|AF117259_1 replication protein [Staphylococcus aureus]
>gi|6690331|gb|AAF24088.1|AF117258_5 hydrolase VgB [Staphylococcus aureus]
>gi|6690330|gb|AAF24087.1|AF117258_4 acetyltransferase Vat [Staphylococcus aureus]
>gi|6690329|gb|AAF24086.1|AF117258_3 resolvase [Staphylococcus aureus]
>gi|6690328|gb|AAF24085.1|AF117258_2 unknown [Staphylococcus aureus]
>gi|6690327|gb|AAF24084.1|AF117258_1 replication protein RepE [Staphylococcus aureus]
>gi|6689210|emb|CAB65404.1| YycJ protein [Staphylococcus aureus]
>gi|6689209|emb|CAB65403.1| YycI protein [Staphylococcus aureus]
>gi|6689208|emb|CAB65402.1| YycH protein [Staphylococcus aureus]
>gi|6689207|emb|CAB65401.1| VicK protein [Staphylococcus aureus]
>gi|6689206|emb|CAB65400.1| TycG protein [Staphylococcus aureus]
>gi|6689205|emb|CAB65399.1| VicR protein [Staphylococcus aureus]
>gi|6681575|dbj|BAA88759.1| cassette chromosome recombinase B [Staphylococcus aureus]
>gi|6681574|dbj|BAA88758.1| cassette chromosome recombinase A [Staphylococcus aureus]
>gi|6681572|dbj|BAA88757.1| cassette chromosome recombinase B [Staphylococcus aureus]
>gi|6681571|dbj|BAA88756.1| cassette chromosome recombinase A [Staphylococcus aureus]
>gi|6681569|dbj|BAA88755.1| cassette chromosome recombinase B [Staphylococcus aureus]
>gi|6681568|dbj|BAA88754.1| cassette chromosome recombinase A [Staphylococcus aureus]
>gi|6644368|gb|AAF21032.1|AF209197_1 UDP-GlcNAc 2-epimerase [Staphylococcus aureus]
>gi|6594284|dbj|BAA88420.1| ATP-binding protein [Staphylococcus aureus]
>gi|6594283|dbj|BAA88419.1| hydrophobic transmembrane protein [Staphylococcus aureus]
>gi|6594281|dbj|BAA88418.1| MsrSA [Staphylococcus aureus]
>gi|6594280|dbj|BAA88417.1| ATP-binding protein [Staphylococcus aureus]
>gi|6594279|dbj|BAA88416.1| hydrophobic transmembrane protein [Staphylococcus aureus]
>gi|6594277|dbj|BAA88415.1| MsrSA [Staphylococcus aureus]
>gi|6594276|dbj|BAA88414.1| ATP-binding protein [Staphylococcus aureus]
>gi|6594275|dbj|BAA88413.1| hydrophobic transmembrane protein [Staphylococcus aureus]
>gi|6578925|gb|AAF18137.1|AF205033_3 glutamyl-tRNAGln amidotransferase subunit B [Staphylococcus aureus]
>gi|6578924|gb|AAF18136.1|AF205033_2 glutamyl-tRNAGln amidotransferase subunit A [Staphylococcus aureus]
>gi|6578923|gb|AAF18135.1|AF205033_1 glutamyl-tRNAGln amidotransferase subunit C [Staphylococcus aureus]
>gi|4185565|gb|AAD09131.1| surface protein Pls [Staphylococcus aureus]
>gi|6492112|gb|AAF14183.1| putative transmembrane protein [Staphylococcus aureus]

>gi|6492111|gb|AAFI4182.1|AFI05976_1 FemX [Staphylococcus aureus]
 >gi|6441050|dbj|BAA86894.1| Drp35 [Staphylococcus aureus]
 >gi|6434054|emb|CAB60756.1| permease [Staphylococcus aureus]
 >gi|6434053|emb|CAB60755.1| ATP-binding protein [Staphylococcus aureus]
 >gi|6434052|emb|CAB60754.1| hypothetical protein [Staphylococcus aureus]
 >gi|6434050|emb|CAB60753.1| anthranilate synthase component II [Staphylococcus aureus]
 >gi|6434049|emb|CAB60752.1| anthranilate phosphoribosyltransferase [Staphylococcus aureus]
 >gi|6434048|emb|CAB60751.1| indole-3-glycerol phosphate synthase [Staphylococcus aureus]
 >gi|6434047|emb|CAB60750.1| phosphoriborylanthranilate isomerase [Staphylococcus aureus]
 >gi|6434045|emb|CAB60749.1| hypothetical protein [Staphylococcus aureus]
 >gi|6434044|emb|CAB60748.1| hypothetical protein [Staphylococcus aureus]
 >gi|6434042|emb|CAB60747.1| hypothetical protein [Staphylococcus aureus]
 >gi|6434041|emb|CAB60746.1| hypothetical protein [Staphylococcus aureus]
 >gi|6434040|emb|CAB60745.1| hypothetical protein [Staphylococcus aureus]
 >gi|6434038|emb|CAB60744.1| hypothetical protein [Staphylococcus aureus]
 >gi|6434037|emb|CAB60743.1| thioredoxine reductase [Staphylococcus aureus]
 >gi|6434035|emb|CAB60742.1| hypothetical protein [Staphylococcus aureus]
 >gi|6434034|emb|CAB60741.1| hypothetical protein [Staphylococcus aureus]
 >gi|6434033|emb|CAB60740.1| thioredoxine reductase [Staphylococcus aureus]
 >gi|6434031|emb|CAB60739.1| porphobilinogen synthase [Staphylococcus aureus]
 >gi|6434030|emb|CAB60738.1| GSA-1-aminotransferase [Staphylococcus aureus]
 >gi|6434029|emb|CAB60737.1| yhjN protein [Staphylococcus aureus]
 >gi|6434028|emb|CAB60736.1| DNA-3-methyladenine glycosidase [Staphylococcus aureus]
 >gi|6273682|emb|CAA73924.1| transposase [Staphylococcus aureus]
 >gi|6273681|emb|CAA73923.1| resolvase [Staphylococcus aureus]
 >gi|6273680|emb|CAA73922.1| hypothetical protein [Staphylococcus aureus]
 >gi|6273679|emb|CAA73921.1| rRNA methylase [Staphylococcus aureus]
 >gi|6273678|emb|CAA73925.1| hypothetical protein [Staphylococcus aureus]
 >gi|6166144|sp|Q53665|DPO3_STAAU DNA POLYMERASE III, ALPHA CHAIN POLC-TYPE (POLIII)
 >gi|3915801|sp|P50073|PARC_STAAU TOPOISOMERASE IV SUBUNIT A
 >gi|2507345|sp|P47770|RPOC_STAAU DNA-DIRECTED RNA POLYMERASE BETA' CHAIN (TRANSCRIPTASE BETA' CHAIN)
 (RNA POLYMERASE BETA' SUBUNIT)
 >gi|135552|sp|P02983|TCR_STAAU TETRACYCLINE RESISTANCE PROTEIN
 >gi|130885|sp|P22490|PRE2_STAAU PLASMID RECOMBINATION ENZYME (MOBILIZATION PROTEIN)
 >gi|128852|sp|P00644|NUC_STAAU THERMONUCLEASE PRECURSOR (TNASE) (MICROCOCCAL NUCLEASE)
 (STAPHYLOCOCCAL NUCLEASE)
 >gi|126941|sp|P26597|MECR_STAEP METHICILLIN RESISTANCE MECR1 PROTEIN
 >gi|6137706|pdb|1QTF|A Chain A, Crystal Structure Of Exfoliative Toxin B
 >gi|4557981|pdb|1SBB|D Chain D, T-Cell Receptor Beta Chain Complexed With Superantigen Seb
 >gi|4557979|pdb|1SBB|B Chain B, T-Cell Receptor Beta Chain Complexed With Superantigen Seb
 >gi|3025223|sp|Q53719|YLY1_STAAU HYPOTHETICAL 18.6 KD PROTEIN IN LYTA 3'REGION (ORF1)
 >gi|2811052|sp|O07319|YLLB_STAAU HYPOTHETICAL 17.4 KD PROTEIN
 >gi|2500373|sp|Q53602|YBXF_STAAU PROBABLE RIBOSOMAL PROTEIN IN RP5L 5'REGION
 >gi|2226349|gb|AAB61744.1| CspC [Staphylococcus aureus]
 >gi|2226347|gb|AAB61743.1| CspB [Staphylococcus aureus]
 >gi|1723202|sp|P55177|YAG5_STAAU HYPOTHETICAL 29.8 KD PROTEIN IN AGR OPERON (ORF 5)
 >gi|1176334|sp|P41370|YIL2_STAAU HYPOTHETICAL PROTEIN IN ILES 3'REGION (ORF C)
 >gi|1176333|sp|P41369|YIL1_STAAU HYPOTHETICAL PROTEIN IN ILES 5'REGION (ORF B)
 >gi|141232|sp|P03860|YPCD_STAAU HYPOTHETICAL 8.7 KD PROTEIN (READING FRAME D)
 >gi|141195|sp|P14503|YP2C_STAAU HYPOTHETICAL 27.7 KD PROTEIN
 >gi|141194|sp|P12052|YP2B_STAAU HYPOTHETICAL 27.0 KD PROTEIN (ORFD)
 >gi|141193|sp|P03866|YP2A_STAAU HYPOTHETICAL 26.9 KD PROTEIN (HYPOTHETICAL PROTEIN C)
 >gi|141190|sp|P23217|YP23_STAAU HYPOTHETICAL TRANSCRIPTIONAL REGULATOR IN QACA 5'REGION (ORF 188)
 >gi|141183|sp|P13977|YP15_STAAU HYPOTHETICAL 15.5 KD PROTEIN
 >gi|141180|sp|P03859|YP12_STAAU HYPOTHETICAL 12.4 KD PROTEIN (READING FRAME C)
 >gi|141043|sp|P08655|YMER_STAAU HYPOTHETICAL 19.7 KD PROTEIN IN MERCURIC RESISTANCE OPERON
 >gi|140780|sp|P21224|YHLB_STAAU HYPOTHETICAL PROTEIN IN HLB 3'REGION
 >gi|1718087|sp|P26839|VATA_STAAU VIRGINIAMYCIN A ACETYLTRANSFERASE
 >gi|138137|sp|P17978|VGB_STAAU VIRGINIAMYCIN B HYDROLASE (VGB)
 >gi|136457|sp|P06886|TSST_STAAU TOXIC SHOCK SYNDROME TOXIN-1 PRECURSOR (TSST-1)
 >gi|6094457|sp|Q53770|TETM_STAAU TETRACYCLINE RESISTANCE PROTEIN TETM (TETA(M))
 >gi|6093662|sp|Q53596|PCP_STAAU PYRROLIDONE-CARBOXYLATE PEPTIDASE (5-OXOPROLYL-PEPTIDASE)
 (PYROGLUTAMYL-PEPTIDASE I) (PGP-I) (PYRASE)
 >gi|3915844|sp|O33276|RRF_STAAU PROBABLE RIBOSOME RECYCLING FACTOR (RIBOSOME RELEASING FACTOR) (RRF)
 >gi|3915057|sp|O32422|SYH_STAAU HISTIDYL-TRNA SYNTHETASE (HISTIDINE--TRNA LIGASE) (HISRS)
 >gi|3914612|sp|O50581|RECG_STAAU ATP-DEPENDENT DNA HELICASE RECG
 >gi|3287914|sp|P81297|STPA_STAAU STAPHOPAIN
 >gi|3122859|sp|O08387|SECY_STAAU PREPROTEIN TRANSLOCASE SECY SUBUNIT
 >gi|3122722|sp|O06444|RL30_STAAU 50S RIBOSOMAL PROTEIN L30
 >gi|3024594|sp|O06442|SECE_STAAU PREPROTEIN TRANSLOCASE SECE SUBUNIT
 >gi|3024540|sp|O06443|RL11_STAAU 50S RIBOSOMAL PROTEIN L11

>gi|3024239|sp|O08386|NUSG_STAAU TRANSCRIPTION ANTITERMINATION PROTEIN NUSG
>gi|2501053|sp|P95689|SYS_STAAU SERYL-TRNA SYNTHETASE (SERINE--TRNA LIGASE) (SERRS)
>gi|2501020|sp|Q53638|SYK_STAAU LYSYL-TRNA SYNTHETASE (LYSINE--TRNA LIGASE) (LYSRS)
>gi|2500269|sp|O06445|RL15_STAAU 50S RIBOSOMAL PROTEIN L15
>gi|1710069|sp|P29232|RECF_STAAU RECF PROTEIN
>gi|1709892|sp|P02907|PTHP_STAAU PHOSPHOCARRIER PROTEIN HPR (HISTIDINE-CONTAINING PROTEIN)
>gi|1709733|sp|P51065|PPCK_STAAU PHOSPHOENOLPYRUVATE CARBOXYKINASE [ATP]
>gi|1709584|sp|P50072|PARE_STAAU TOPOISOMERASE IV SUBUNIT B
>gi|1709245|sp|P50588|NDK_STAAU NUCLEOSIDE DIPHOSPHATE KINASE (NDK) (NDP KINASE)
>gi|1351009|sp|P48940|RS7_STAAU 30S RIBOSOMAL PROTEIN S7
>gi|1350927|sp|P48942|RS12_STAAU 30S RIBOSOMAL PROTEIN S12
>gi|1350849|sp|P47768|RPOB_STAAU DNA-DIRECTED RNA POLYMERASE BETA CHAIN (TRANSCRIPTASE BETA CHAIN) (RNA POLYMERASE BETA SUBUNIT)
>gi|1350771|sp|P48860|RL7_STAAU 50S RIBOSOMAL PROTEIN L7/L12
>gi|1346789|sp|P03864|PRE3_STAAU PLASMID RECOMBINATION ENZYME (MOBILIZATION PROTEIN)
>gi|1346788|sp|P03857|PRE1_STAAU PLASMID RECOMBINATION ENZYME (MOBILIZATION PROTEIN)
>gi|1175774|sp|P45557|PRMA_STAAU PROBABLE METHYLTRANSFERASE
>gi|1174516|sp|P41368|SYIP_STAAU ISOLEUCYL-TRNA SYNTHETASE, MUPIROCIN RESISTANT (ISOLEUCINE--TRNA LIGASE) (ILERS) (MUPIROCIN RESISTANCE PROTEIN)
>gi|1172527|sp|P45723|PLC_STAAU 1-PHOSPHATIDYLINOSITOL PHOSPHODIESTERASE PRECURSOR (PHOSPHATIDYLINOSITOL-SPECIFIC PHOSPHOLIPASE C) (PI-PLC)
>gi|586104|sp|P37376|TNPF_STAAU TRANSPOSASE FOR TRANSPOSON TN554 HOMOLOG
>gi|586103|sp|P37375|TNPE_STAAU TRANSPOSASE B (TRANSPOSON TN554 HOMOLOG)
>gi|586027|sp|P38507|SPA2_STAAU IMMUNOGLOBULIN G BINDING PROTEIN A PRECURSOR (IGG BINDING PROTEIN A)
>gi|548620|sp|P17875|PTMA_STAAU PTS SYSTEM, MANNITOL-SPECIFIC IIA COMPONENT (EIIA-MTL) (MANNITOL-PERMEASE IIA COMPONENT) (PHOSPHOTRANSFERASE ENZYME II, A COMPONENT) (EIII-MTL)
>gi|548619|sp|PTMA_STAAU_2 [Segment 2 of 2] PTS SYSTEM, MANNITOL-SPECIFIC IIA COMPONENT (EIIA-MTL) (MANNITOL-PERMEASE IIA COMPONENT) (PHOSPHOTRANSFERASE ENZYME II, A COMPONENT) (EIII-MTL)
>gi|548618|sp|PTMA_STAAU_1 [Segment 1 of 2] PTS SYSTEM, MANNITOL-SPECIFIC IIA COMPONENT (EIIA-MTL) (MANNITOL-PERMEASE IIA COMPONENT) (PHOSPHOTRANSFERASE ENZYME II, A COMPONENT) (EIII-MTL)
>gi|400965|sp|P31337|RADC_STAAU DNA REPAIR PROTEIN RADC HOMOLOG (25 KD PROTEIN)
>gi|136146|sp|P06698|TRAC_STAAU TRANSPOSASE FOR TRANSPOSON TN554
>gi|136133|sp|P18416|TRA3_STAAU TRANSPOSASE FOR TRANSPOSON TN552 (ORF 480)
>gi|135956|sp|P06697|TNPB_STAAU TRANSPOSASE B (TRANSPOSON TN554)
>gi|135955|sp|P06696|TNPA_STAAU TRANSPOSASE A (TRANSPOSON TN554)
>gi|135949|sp|P19775|TRA6_STAAU TRANSPOSASE FOR INSERTION SEQUENCE ELEMENT IS256 IN TRANSPOSON TN4001
>gi|135248|sp|P23736|T2S9_STAAU TYPE II RESTRICTION ENZYME SAU96I (ENDONUCLEASE SAU96I) (R.SAU96I)
>gi|135247|sp|P16667|T2S3_STAAU TYPE II RESTRICTION ENZYME SAU3AI (ENDONUCLEASE SAU3AI) (R.SAU3AI)
>gi|135003|sp|P04188|TSP_STAAU GLUTAMYL ENDOPEPTIDASE PRECURSOR (STAPHYLOCOCCAL SERINE PROTEINASE) (V8 PROTEINASE) (ENDOPROTEINASE GLU-C)
>gi|135002|sp|P12055|STR_STAAU STREPTOMYCIN RESISTANCE PROTEIN
>gi|134959|sp|P17855|STC2_STAAU STAPHYLOCOAGULASE PRECURSOR
>gi|134958|sp|P07767|STC1_STAAU STAPHYLOCOAGULASE PRECURSOR
>gi|134189|sp|P00802|SAK_STAAU STAPHYLOKINASE PRECURSOR (NEUTRAL PROTEINASE) (PROTEASE III)
>gi|134150|sp|P04827|S3AD_STAAU STREPTOMYCIN 3''-ADENYLYLTRANSFERASE (AAD(9))
>gi|133479|sp|P26766|RPSD_STAAU RNA POLYMERASE SIGMA FACTOR RPOD
>gi|133112|sp|P14491|RLX3_STAAU RLX PROTEIN
>gi|133111|sp|P03865|RLX2_STAAU RLX PROTEIN
>gi|133109|sp|P12054|RLX1_STAAU RLX PROTEIN
>gi|132380|sp|P08115|REP_STAAU REPLICATION INITIATION PROTEIN
>gi|132374|sp|P03858|REPY_STAAU REPLICATION PROTEIN
>gi|132372|sp|P03862|REPX_STAAU REP PROTEIN (REPLICATION PROTEIN) (READING FRAME A)
>gi|132369|sp|P19529|REPN_STAAU REPLICATION INITIATION PROTEIN
>gi|132368|sp|P14490|REPM_STAAU REPLICATION INITIATION PROTEIN
>gi|132364|sp|P12053|REPE_STAAU REPLICATION INITIATION PROTEIN
>gi|132362|sp|P03065|REPD_STAAU REPLICATION INITIATION PROTEIN
>gi|132361|sp|P03064|REPC_STAAU REPLICATION INITIATION PROTEIN (PROTEIN A)
>gi|132357|sp|P05061|REPB_STAAU REPLICATION PROTEIN
>gi|132322|sp|P13969|REMA_STAAU REPLICATION AND MAINTENANCE PROTEIN (PLASMID REPLICATION PROTEIN)
>gi|131518|sp|P02909|PTLA_STAAU PTS SYSTEM, LACTOSE-SPECIFIC IIA COMPONENT (EIIA-LAC) (LACTOSE-PERMEASE IIA COMPONENT) (PHOSPHOTRANSFERASE ENZYME II, A COMPONENT) (EIII-LAC)
>gi|131497|sp|P11162|PTLB_STAAU PTS SYSTEM, LACTOSE-SPECIFIC IIBC COMPONENT (EIIBC-LAC) (LACTOSE-PERMEASE IIBC COMPONENT) (PHOSPHOTRANSFERASE ENZYME II, BC COMPONENT) (EII-LAC)
>gi|130085|sp|P09978|PHLC_STAAU PHOSPHOLIPASE C PRECURSOR (BETA-HEMOLYSIN) (BETA-TOXIN) (SPHINGOMYELINASE)
>gi|129676|sp|P07944|PBP_STAAU BETA-LACTAM-INDUCIBLE PENICILLIN-BINDING PROTEIN
>gi|129132|sp|P21223|OMP7_STAAU 70 KD OUTER MEMBRANE PROTEIN PRECURSOR
>gi|129123|sp|P21222|NP30_STAAU 30 KD NEUTRAL PHOSPHATASE (NPTASE)
>gi|128511|sp|P21191|NORA_STAAU QUINOLONE RESISTANCE NORA PROTEIN

>gi|127486|sp|P23737|MTS9_STAAU MODIFICATION METHYLASE SAU96I (CYTOSINE-SPECIFIC METHYLTRANSFERASE SAU96I) (M.SAU96I)
>gi|127485|sp|P16668|MTS3_STAAU MODIFICATION METHYLASE SAU3AI (CYTOSINE-SPECIFIC METHYLTRANSFERASE SAU3AI) (M.SAU3AI)
>gi|6016606|sp|P068285|MSCL_STAAU LARGE-CONDUCTANCE MECHANOTENSITIVE CHANNEL
>gi|6016162|sp|P034092|GSA_STAAU GLUTAMATE-1-SEMIALDEHYDE 2,1-AMINOMUTASE (GSA) (GLUTAMATE-1-SEMIALDEHYDE AMINOTRANSFERASE) (GSA-AT)
>gi|4033454|sp|P72364|LEPH_STAAU INACTIVE SIGNAL PEPTIDASE IA
>gi|4033452|sp|P72365|LEP_STAAU SIGNAL PEPTIDASE IB (SPASE IB) (LEADER PEPTIDASE IB)
>gi|3122102|sp|P007325|FTSA_STAAU CELL DIVISION PROTEIN FTSA
>gi|1709003|sp|P50307|METK_STAAU S-ADENOSYLMETHIONINE SYNTHETASE (METHIONINE ADENOSYLTRANSFERASE) (ADOMET SYNTHETASE)
>gi|1708807|sp|P52282|LGT_STAAU PROLIPOPROTEIN DIACYLGLYCERYL TRANSFERASE
>gi|1707902|sp|P31714|GHM2_STAAU GAMMA-HEMOLYSIN H-GAMMA-II SUBUNIT
>gi|1707901|sp|GHM2_STAAU_2 [Segment 2 of 2] GAMMA-HEMOLYSIN H-GAMMA-II SUBUNIT
>gi|1707900|sp|GHM2_STAAU_1 [Segment 1 of 2] GAMMA-HEMOLYSIN H-GAMMA-II SUBUNIT
>gi|1346584|sp|P80544|MRSP_STAAU METHICILLIN-RESISTANT SURFACE PROTEIN
>gi|1346583|sp|MRSP_STAAU_7 [Segment 7 of 7] METHICILLIN-RESISTANT SURFACE PROTEIN
>gi|1346582|sp|MRSP_STAAU_6 [Segment 6 of 7] METHICILLIN-RESISTANT SURFACE PROTEIN
>gi|1346581|sp|MRSP_STAAU_5 [Segment 5 of 7] METHICILLIN-RESISTANT SURFACE PROTEIN
>gi|1346580|sp|MRSP_STAAU_4 [Segment 4 of 7] METHICILLIN-RESISTANT SURFACE PROTEIN
>gi|1346579|sp|MRSP_STAAU_3 [Segment 3 of 7] METHICILLIN-RESISTANT SURFACE PROTEIN
>gi|1346578|sp|MRSP_STAAU_2 [Segment 2 of 7] METHICILLIN-RESISTANT SURFACE PROTEIN
>gi|1346577|sp|MRSP_STAAU_1 [Segment 1 of 7] METHICILLIN-RESISTANT SURFACE PROTEIN
>gi|1346244|sp|P20832|GYRB_STAAU DNA GYRASE SUBUNIT B
>gi|1346238|sp|P20831|GYRA_STAAU DNA GYRASE SUBUNIT A
>gi|1176137|sp|P45556|HRCA_STAAU HEAT-INDUCIBLE TRANSCRIPTION REPRESSOR HRCA
>gi|1169769|sp|P45498|FTSZ_STAAU CELL DIVISION PROTEIN FTSZ
>gi|547868|sp|P36884|LPCA_STAAU CHLORAMPHENICOL RESISTANCE LEADER PEPTIDE
>gi|400204|sp|P31716|LUKS_STAAU LEUKOCIDIN S SUBUNIT PRECURSOR
>gi|400203|sp|P31715|LUKF_STAAU LEUKOCIDIN F SUBUNIT PRECURSOR (GAMMA-HEMOLYSIN, H-GAMMA-I SUBUNIT)
>gi|127020|sp|P08656|MERT_STAAU MERCURIC TRANSPORT PROTEIN (MERCURY ION TRANSPORT PROTEIN)
>gi|127015|sp|P22874|MERR_STAAU MERCURIC RESISTANCE OPERON REGULATORY PROTEIN
>gi|126999|sp|P08653|MERR_STAAU ALKYL MERCURY LYASE (ORGANOMERCURIAL LYASE)
>gi|126995|sp|P08663|MERA_STAAU MERCURIC REDUCTASE (HG(II) REDUCTASE)
>gi|126940|sp|P26598|MERC1_STAAU METHICILLIN RESISTANCE REGULATORY PROTEIN MECI
>gi|126446|sp|P03063|LPRM_STAAU 23S RNA METHYLASE LEADER PEPTIDE (ERYTHROMYCIN RESISTANCE LEADER PEPTIDE)
>gi|126333|sp|P10335|LIP_STAAU LIPASE PRECURSOR (GLYCEROL ESTER HYDROLASE)
>gi|125937|sp|P16644|LACR_STAAU LACTOSE PHOSPHOTRANSFERASE SYSTEM REPRESSOR
>gi|125930|sp|P11175|LACG_STAAU 6-PHOSPHO-BETA-GALACTOSIDASE (BETA-D-PHOSPHOGALACTOSIDE GALACTOHYDROLASE) (PGALASE) (P-BETA-GAL) (PBG)
>gi|125908|sp|P26594|LACA_STAAU GALACTOSE-6-PHOSPHATE ISOMERASE LACA SUBUNIT
>gi|125464|sp|P00554|KKA3_ENTFA AMINOGLYCOSIDE 3'-PHOSPHOTRANSFERASE (KANAMYCIN KINASE, TYPE III) (NEOMYCIN-KANAMYCIN PHOSPHOTRANSFERASE, TYPE III) (APH(3')III)
>gi|125191|sp|P05057|KANU_STAAU KANAMYCIN NUCLEOTIDYLTRANSFERASE (NEO(R))
>gi|123184|sp|P09616|HLA_STAAU ALPHA-HEMOLYSIN PRECURSOR (ALPHA-TOXIN) (ALPHA-HL)
>gi|6015099|sp|P069174|ENO_STAAU ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (LAMININ BINDING PROTEIN)
>gi|6014977|sp|P059822|DLDH_STAAU DIHYDROLIPOAMIDE DEHYDROGENASE (E3 COMPONENT OF PYRUVATE COMPLEX) (MEMBRANE-BOUND RIBOSOME PROTEIN COMPLEX 50 KD SUBUNIT)
>gi|6014729|sp|P81684|CS40_STAAU 40 KD VITRONECTIN-BINDING CELL SURFACE PROTEIN
>gi|3023644|sp|P005701|DHP5_STAAU DIHYDROPTEROATE SYNTHASE (DIHYDROPTEROATE PYROPHOSPHORYLASE) (DHP5)
>gi|2829402|sp|P49994|DNAA_STAAU CHROMOSOMAL REPLICATION INITIATOR PROTEIN DNAA
>gi|1706496|sp|P50029|DP3B_STAAU DNA POLYMERASE III, BETA CHAIN
>gi|1169381|sp|P45554|DNAK_STAAU DNAK PROTEIN (HEAT SHOCK PROTEIN 70) (HSP70)
>gi|544199|sp|P10167|DYRB_STAAU DIHYDROFOLATE REDUCTASE TYPE I
>gi|462026|sp|P34071|ETC2_STAAU ENTEROTOXIN TYPE C-2 PRECURSOR (SEC2)
>gi|127195|sp|P13978|ERM4_STAAU RNA ADENINE N-6-METHYLTRANSFERASE (MACROLIDE-LINCOSAMIDE-STREPTOGRAMIN B RESISTANCE PROTEIN) (ERYTHROMYCIN RESISTANCE PROTEIN)
>gi|127194|sp|P13957|ERM3_STAAU RNA ADENINE N-6-METHYLTRANSFERASE (MACROLIDE-LINCOSAMIDE-STREPTOGRAMIN B RESISTANCE PROTEIN) (ERYTHROMYCIN RESISTANCE PROTEIN)
>gi|127191|sp|P06699|ERM1_STAAU RNA ADENINE N-6-METHYLTRANSFERASE (MACROLIDE-LINCOSAMIDE-STREPTOGRAMIN B RESISTANCE PROTEIN) (ERYTHROMYCIN RESISTANCE PROTEIN)
>gi|119903|sp|P14305|FEMB_STAAU POSSIBLE PROTEIN FEMB (ORF 419)
>gi|119902|sp|P14304|FEMA_STAAU FACTOR ESSENTIAL FOR EXPRESSION OF METHICILLIN RESISTANCE
>gi|119655|sp|P12993|ETXE_STAAU ENTEROTOXIN TYPE E PRECURSOR (SEE)
>gi|119654|sp|P20723|ETXD_STAAU ENTEROTOXIN TYPE D PRECURSOR (SED)
>gi|119653|sp|P01552|ETXB_STAAU ENTEROTOXIN TYPE B PRECURSOR (SEB)
>gi|119652|sp|P13163|ETXA_STAAU ENTEROTOXIN TYPE A PRECURSOR (SEA)
>gi|119626|sp|P23313|ETC3_STAAU ENTEROTOXIN TYPE C-3 PRECURSOR (SEC3)

>gi|119625|sp|P01553|ETC1_STAAU ENTEROTOXIN TYPE C-1 PRECURSOR (SEC1)
 >gi|119624|sp|P09332|ETB_STAAU EXFOLIATIVE TOXIN B PRECURSOR (EPIDERMOLYTIC TOXIN B)
 >gi|119621|sp|P09331|ETA_STAAU EXFOLIATIVE TOXIN A PRECURSOR (EPIDERMOLYTIC TOXIN A)
 >gi|119131|sp|P24121|EDIN_STAAU EPIDERMAL CELL DIFFERENTIATION INHIBITOR PRECURSOR (EDIN)
 >gi|118976|sp|P13955|DYRA_STAAU DIHYDROFOLATE REDUCTASE TYPE I (TN4003)
 >gi|5813905|gb|AAD52059.1|AF086783_7 glycerol esther hydrolase [Staphylococcus aureus]
 >gi|5813904|gb|AAD52058.1|AF086783_6 IcaC [Staphylococcus aureus]
 >gi|5813903|gb|AAD52057.1|AF086783_5 IcaB [Staphylococcus aureus]
 >gi|5813902|gb|AAD52056.1|AF086783_4 IcaD [Staphylococcus aureus]
 >gi|5813901|gb|AAD52055.1|AF086783_3 IcaA [Staphylococcus aureus]
 >gi|5813900|gb|AAD52054.1|AF086783_2 IcaR [Staphylococcus aureus]
 >gi|5813899|gb|AAD52053.1|AF086783_1 CapA [Staphylococcus aureus]
 >gi|6002652|gb|AAF00080.1|AF095597_1 ferric uptake regulator homolog [Staphylococcus aureus]
 >gi|6002650|gb|AAF00079.1|AF095596_1 ferric uptake regulator homolog [Staphylococcus aureus]
 >gi|6002648|gb|AAF00078.1|AF095595_1 ferric uptake regulator homolog [Staphylococcus aureus]
 >gi|3913259|sp|Q53654|CNA_STAAU COLLAGEN ADHESIN PRECURSOR
 >gi|584919|sp|Q08841|CH10_STAAU 10 KD CHAPERONIN (PROTEIN CPN10) (PROTEIN GROES) (HEAT SHOCK PROTEIN 10)
 >gi|116920|sp|P25921|COP6_STAAU COP-6 PROTEIN
 >gi|1168660|sp|P20384|BIN3_STAAU POTENTIAL DNA-INVERTASE BIN3 (TRANSPOSON TN552)
 >gi|729029|sp|P39861|CAPL_STAAU CAPL PROTEIN
 >gi|729028|sp|P39860|CAPK_STAAU CAPK PROTEIN
 >gi|729027|sp|P39859|CAPJ_STAAU CAPJ PROTEIN
 >gi|729025|sp|P39857|CAPH_STAAU CAPH PROTEIN
 >gi|729024|sp|P39856|CAPG_STAAU CAPG PROTEIN
 >gi|729021|sp|P39855|CAPF_STAAU CAPF PROTEIN
 >gi|729020|sp|P39854|CAPE_STAAU CAPE PROTEIN
 >gi|729019|sp|P39853|CAPD_STAAU CAPD PROTEIN
 >gi|729018|sp|P39852|CAPC_STAAU CAPC PROTEIN
 >gi|729017|sp|P39851|CAPB_STAAU CAPB PROTEIN
 >gi|729016|sp|P39850|CAPA_STAAU CAPA PROTEIN
 >gi|584871|sp|P37374|CADF_STAAU CADMIUM EFFLUX SYSTEM ACCESSORY PROTEIN HOMOLOG
 >gi|584870|sp|P37386|CADD_STAAU PROBABLE CADMIUM-TRANSPORTING ATPASE (CADMIUM EFFLUX ATPASE)
 >gi|543935|sp|P36883|CAT5_STAAU CHLORAMPHENICOL ACETYLTRANSFERASE
 >gi|543934|sp|P36882|CAT4_STAAU CHLORAMPHENICOL ACETYLTRANSFERASE
 >gi|231569|sp|P30338|ARSR_STAAU ARSENICAL RESISTANCE OPERON REPRESSOR
 >gi|231567|sp|P30330|ARSC_STAAU ARSENATE REDUCTASE (ARSENICAL PUMP MODIFIER)
 >gi|231565|sp|P30329|ARSB_STAAU ARSENICAL PUMP MEMBRANE PROTEIN
 >gi|140340|sp|P20047|CADC_STAAU CADMIUM EFFLUX SYSTEM ACCESSORY PROTEIN
 >gi|115688|sp|P06135|CAT3_STAAU CHLORAMPHENICOL ACETYLTRANSFERASE
 >gi|115685|sp|P00486|CAT2_STAAU CHLORAMPHENICOL ACETYLTRANSFERASE
 >gi|115680|sp|P00485|CAT1_STAAU CHLORAMPHENICOL ACETYLTRANSFERASE
 >gi|115414|sp|P20021|CADA_STAAU PROBABLE CADMIUM-TRANSPORTING ATPASE (CADMIUM EFFLUX ATPASE)
 >gi|115052|sp|P22491|BLE2_STAAU BLEOMYCIN RESISTANCE PROTEIN
 >gi|115051|sp|P13014|BLE1_BACSP BLEOMYCIN RESISTANCE PROTEIN (BRP)
 >gi|115049|sp|P18357|BLAR_STAAU REGULATORY PROTEIN BLAR1
 >gi|115044|sp|P18415|BLAI_STAAU PENICILLINASE REPRESSOR (REGULATORY PROTEIN BLAI) (BETA-LACTAMASE REPRESSOR PROTEIN)
 >gi|114996|sp|P19241|BINR_STAAU DNA-INVERTASE BINR (TRANSPOSON TN552)
 >gi|114995|sp|P18358|BINL_STAAU TRANSPOSON TN552 RESOLVASE
 >gi|114300|sp|P18179|ATBP_STAAU POTENTIAL ATP-BINDING PROTEIN (ORF 271)
 >gi|3913011|sp|O05204|AHFF_STAAU ALKYL HYDROPEROXIDE REDUCTASE SUBUNIT F
 >gi|113527|sp|P13131|AGRA_STAAU ACCESSORY GENE REGULATOR PROTEIN A
 >gi|112954|sp|P14507|AACA_STAAU BIFUNCTIONAL AAC/APH [INCLUDES: 6'-AMINOGLYCOSIDE N-ACETYLTRANSFERASE (AAC(6'))]; 2''-AMINOGLYCOSIDE PHOSPHOTRANSFERASE (APH(2''))]
 >gi|1729798|emb|CAA71069.1| CTORF239 [Staphylococcus aureus]
 >gi|1729797|emb|CAA71068.1| sigma-B [Staphylococcus aureus]
 >gi|1729796|emb|CAA71067.1| rsbW [Staphylococcus aureus]
 >gi|1729795|emb|CAA71066.1| rsbV [Staphylococcus aureus]
 >gi|1729794|emb|CAA71065.1| rsbU [Staphylococcus aureus]
 >gi|1729793|emb|CAA71064.1| ORF136 [Staphylococcus aureus]
 >gi|1729792|emb|CAA71063.1| ORF56 [Staphylococcus aureus]
 >gi|5834651|emb|CAB55331.1| putative mannitol-specific IIA component [Staphylococcus aureus]
 >gi|5834650|emb|CAB55330.1| putative mannitol-1-phosphate 5-dehydrogenase [Staphylococcus aureus]
 >gi|5834649|emb|CAB55329.1| Mrp protein [Staphylococcus aureus]
 >gi|5834648|emb|CAA71060.2| phosphoglucosamine mutase, GlmM [Staphylococcus aureus]
 >gi|5834647|emb|CAB55328.1| hypothetical protein [Staphylococcus aureus]
 >gi|5834646|emb|CAB55327.1| hypothetical protein [Staphylococcus aureus]
 >gi|5834645|emb|CAB55326.1| arginase [Staphylococcus aureus]
 >gi|4775551|emb|CAA71062.1| CTORF1365 [Staphylococcus aureus]
 >gi|4775543|emb|CAA70781.1| arginase [Staphylococcus aureus]

>gi|4574235|gb|AAD23961.1|AF106850_1 FmhB [Staphylococcus aureus]
>gi|4574233|gb|AAD23960.1|AF106849_1 FmhA [Staphylococcus aureus]
>gi|4572581|gb|AAD15142.2| Unknown [Staphylococcus aureus]
>gi|3891901|pdb|1CV8| Staphopain, Cysteine Proteinase From Staphylococcus Aureus V8
>gi|2981905|pdb|3NUC| Staphylococcal Nuclease, 1-N-Propane Thiol Disulfide To V23c Variant
>gi|2981899|pdb|2NUC| Staphylococcal Nuclease, Ethane Thiol Disulfide To V23c Variant
>gi|1942332|pdb|1SNQ| Protein Stability In Staphylococcal Nuclease
>gi|1942331|pdb|1SNP| Protein Stability In Staphylococcal Nuclease
>gi|1942330|pdb|1SNO| Protein Stability In Staphylococcal Nuclease
>gi|4139848|pdb|1SSN| Staphylokinase, Sakstar Variant, Nmr, 20 Structures
>gi|4139648|pdb|1TS5|B Chain B, I140t Mutant Of Toxic Shock Syndrome Toxin-1 From S. Aureus
>gi|4139647|pdb|1TS5|A Chain A, I140t Mutant Of Toxic Shock Syndrome Toxin-1 From S. Aureus
>gi|4139646|pdb|1TS4|B Chain B, Q139k Mutant Of Toxic Shock Syndrome Toxin-1 From S. Aureus
>gi|4139645|pdb|1TS4|A Chain A, Q139k Mutant Of Toxic Shock Syndrome Toxin-1 From S. Aureus
>gi|4139644|pdb|1TS3|C Chain C, H135a Mutant Of Toxic Shock Syndrome Toxin-1 From S. Aureus
>gi|4139643|pdb|1TS3|B Chain B, H135a Mutant Of Toxic Shock Syndrome Toxin-1 From S. Aureus
>gi|4139642|pdb|1TS3|A Chain A, H135a Mutant Of Toxic Shock Syndrome Toxin-1 From S. Aureus
>gi|4139641|pdb|1TS2|C Chain C, T128a Mutant Of Toxic Shock Syndrome Toxin-1 From S. Aureus
>gi|4139640|pdb|1TS2|B Chain B, T128a Mutant Of Toxic Shock Syndrome Toxin-1 From S. Aureus
>gi|4139639|pdb|1TS2|A Chain A, T128a Mutant Of Toxic Shock Syndrome Toxin-1 From S. Aureus
>gi|3891592|pdb|1AW7|D Chain D, Q136a Mutant Of Toxic Shock Syndrome Toxin-1 From S. Aureus
>gi|3891591|pdb|1AW7|C Chain C, Q136a Mutant Of Toxic Shock Syndrome Toxin-1 From S. Aureus
>gi|3891590|pdb|1AW7|B Chain B, Q136a Mutant Of Toxic Shock Syndrome Toxin-1 From S. Aureus
>gi|3891589|pdb|1AW7|A Chain A, Q136a Mutant Of Toxic Shock Syndrome Toxin-1 From S. Aureus
>gi|4454324|emb|CAA10802.1| MapN protein [Staphylococcus aureus]
>gi|3970797|emb|CAA74099.1| polynucleotide phosphorylase [Staphylococcus aureus]
>gi|4530244|gb|AAD21960.1| putative exoprotein DltD [Staphylococcus aureus]
>gi|4530243|gb|AAD21959.1| D-alanine carrier protein DltC [Staphylococcus aureus]
>gi|4530242|gb|AAD21958.1| putative membrane protein DltB [Staphylococcus aureus]
>gi|4530241|gb|AAD21957.1| D-alanine-D-alanyl carrier protein ligase DltA [Staphylococcus aureus]
>gi|4530240|gb|AAD21956.1| unknown [Staphylococcus aureus]
>gi|4490615|emb|CAB38647.1| triosephosphate isomerase [Staphylococcus aureus]
>gi|4490614|emb|CAB38646.1| phosphoglycerate kinase [Staphylococcus aureus]
>gi|4490613|emb|CAB38645.1| glyceraldehyde-3-phosphate dehydrogenase [Staphylococcus aureus]
>gi|4490612|emb|CAB38644.1| gap regulator [Staphylococcus aureus]
>gi|4490610|emb|CAB38643.1| ribonucleotide reductase minor subunit [Staphylococcus aureus]
>gi|4490609|emb|CAB38642.1| ribonucleotide reductase major subunit [Staphylococcus aureus]
>gi|4490608|emb|CAB38641.1| NRDL [Staphylococcus aureus]
>gi|4454322|emb|CAA10788.1| hypothetical protein [Staphylococcus aureus]
>gi|4454321|emb|CAA10787.1| hypothetical protein [Staphylococcus aureus]
>gi|4126675|dbj|BAA36689.1| Hypothetical protein [Staphylococcus aureus]
>gi|4126674|dbj|BAA36688.1| Hypothetical protein [Staphylococcus aureus]
>gi|4126673|dbj|BAA36687.1| CzrA [Staphylococcus aureus]
>gi|4126672|dbj|BAA36686.1| czcD [Staphylococcus aureus]
>gi|4126671|dbj|BAA36685.1| Hypothetical protein [Staphylococcus aureus]
>gi|4001731|dbj|BAA35101.1| MnhG [Staphylococcus aureus]
>gi|4001730|dbj|BAA35100.1| MnhF [Staphylococcus aureus]
>gi|4001729|dbj|BAA35099.1| MnhE [Staphylococcus aureus]
>gi|4001728|dbj|BAA35098.1| MnhD [Staphylococcus aureus]
>gi|4001727|dbj|BAA35097.1| MnhC [Staphylococcus aureus]
>gi|4001726|dbj|BAA35096.1| MnhB [Staphylococcus aureus]
>gi|4001725|dbj|BAA35095.1| MnhA [Staphylococcus aureus]
>gi|4001724|dbj|BAA35094.1| OrfA [Staphylococcus aureus]
>gi|3694944|gb|AAC62498.1| SirC [Staphylococcus aureus]
>gi|3694943|gb|AAC62497.1| SirB [Staphylococcus aureus]
>gi|3694942|gb|AAC62496.1| lipoprotein SirA [Staphylococcus aureus]
>gi|4138456|emb|CAA11555.1| Map protein [Staphylococcus aureus]
>gi|4138445|emb|CAA77018.1| adenine methylase [Staphylococcus aureus]
>gi|3955031|emb|CAA76853.1| PBP2 [Staphylococcus aureus]
>gi|3955030|emb|CAA76852.1| unknown [Staphylococcus aureus]
>gi|3550596|emb|CAA06652.1| sdr E [Staphylococcus aureus]
>gi|3550594|emb|CAA06651.1| sdrD [Staphylococcus aureus]
>gi|3550592|emb|CAA06650.1| sdrC [Staphylococcus aureus]
>gi|809080|emb|CAA24595.1| reading frame [Staphylococcus aureus]
>gi|3320606|gb|AAD09875.1| putative heme A synthase [Staphylococcus aureus]
>gi|4104230|gb|AAD01977.1| phospho-N-acetylmuramoyl-pentapeptide translocase [Staphylococcus aureus]
>gi|4103900|gb|AAD01884.1| 60 kDa heat shock protein [Staphylococcus aureus]
>gi|4097757|gb|AAD00167.1| lytic regulatory protein [Staphylococcus aureus]
>gi|4090655|gb|AAC98834.1| ORF64 [Staphylococcus aureus]
>gi|4090654|gb|AAC98833.1| replication protein [Staphylococcus aureus]
>gi|4090652|gb|AAC98832.1| ORF64 [Staphylococcus aureus]

>gi|4090651|gb|AAC98831.1| replication protein [Staphylococcus aureus]
 >gi|2811118|gb|AAC95492.1| unknown [Staphylococcus aureus]
 >gi|2811115|gb|AAC95491.1| unknown [Staphylococcus aureus]
 >gi|4009497|gb|AAC95464.1| cell division protein DivIVA [Staphylococcus aureus]
 >gi|4009496|gb|AAC95463.1| YlmH [Staphylococcus aureus]
 >gi|4009495|gb|AAC95462.1| YlmG [Staphylococcus aureus]
 >gi|4009494|gb|AAC95461.1| YlmF [Staphylococcus aureus]
 >gi|4009493|gb|AAC95460.1| YlmE [Staphylococcus aureus]
 >gi|4009492|gb|AAC95459.1| YlmD [Staphylococcus aureus]
 >gi|4009491|gb|AAC95458.1| cell division protein FtsZ [Staphylococcus aureus]
 >gi|1402771|gb|AAC80254.1| major cold-shock protein [Staphylococcus aureus]
 >gi|3372542|gb|AAC78590.1| enterotoxin J [Staphylococcus aureus]
 >gi|3372541|gb|AAC78589.1| enterotoxin D [Staphylococcus aureus]
 >gi|3892644|dbj|BAA34540.1| MphBM [Staphylococcus aureus]
 >gi|3892643|dbj|BAA34539.1| MsrSA [Staphylococcus aureus]
 >gi|3892642|dbj|BAA34538.1| leader peptide [Staphylococcus aureus]
 >gi|3850852|emb|CAA76222.1| hypothetical protein [Staphylococcus aureus]
 >gi|3850851|emb|CAA76221.1| alr protein [Staphylococcus aureus]
 >gi|3850850|emb|CAA76220.1| dpj protein [Staphylococcus aureus]
 >gi|3850849|emb|CAA76219.1| hypothetical protein [Staphylococcus aureus]
 >gi|3850848|emb|CAA76218.1| hypothetical protein [Staphylococcus aureus]
 >gi|3850847|emb|CAA76217.1| hypothetical protein [Staphylococcus aureus]
 >gi|3850846|emb|CAA76216.1| kpdC protein [Staphylococcus aureus]
 >gi|3800828|gb|AAC69846.1| oligopeptide transporter putative ATPase domain [Staphylococcus aureus]
 >gi|3800827|gb|AAC69845.1| oligopeptide transporter putative ATPase domain [Staphylococcus aureus]
 >gi|3800826|gb|AAC69844.1| oligopeptide transporter putative membrane permease domain [Staphylococcus aureus]
 >gi|3800825|gb|AAC69843.1| oligopeptide transporter putative membrane permease domain [Staphylococcus aureus]
 >gi|3800823|gb|AAC69842.1| unknown [Staphylococcus aureus]
 >gi|3800822|gb|AAC69841.1| oligopeptide transporter putative ATPase domain [Staphylococcus aureus]
 >gi|3800821|gb|AAC69840.1| oligopeptide transporter putative ATPase domain [Staphylococcus aureus]
 >gi|3800820|gb|AAC69839.1| oligopeptide transporter putative membrane permease domain [Staphylococcus aureus]
 >gi|3800819|gb|AAC69838.1| oligopeptide transporter putative membrane permease domain [Staphylococcus aureus]
 >gi|3800818|gb|AAC69837.1| oligopeptide transporter putative substrate binding domain [Staphylococcus aureus]
 >gi|2765304|emb|CAA73668.1| leukotoxin, LukD [Staphylococcus aureus]
 >gi|2765303|emb|CAA73667.1| leukotoxin Luke [Staphylococcus aureus]
 >gi|3212829|pdb|5NUC| Staphylococcal Nuclease, 1-N-Pentane Thiol Disulfide To V23c Variant
 >gi|3212819|pdb|3SEB| Staphylococcal Enterotoxin B
 >gi|2982145|pdb|2SAK| Staphylokinase (Sakstar Variant)
 >gi|2914575|pdb|7AHL|G Chain G, Alpha-Hemolysin From Staphylococcus Aureus
 >gi|2914574|pdb|7AHL|F Chain F, Alpha-Hemolysin From Staphylococcus Aureus
 >gi|2914573|pdb|7AHL|E Chain E, Alpha-Hemolysin From Staphylococcus Aureus
 >gi|2914572|pdb|7AHL|D Chain D, Alpha-Hemolysin From Staphylococcus Aureus
 >gi|2914571|pdb|7AHL|C Chain C, Alpha-Hemolysin From Staphylococcus Aureus
 >gi|2914570|pdb|7AHL|B Chain B, Alpha-Hemolysin From Staphylococcus Aureus
 >gi|2914569|pdb|7AHL|A Chain A, Alpha-Hemolysin From Staphylococcus Aureus
 >gi|2914205|pdb|2SEB|D Chain D, X-Ray Crystal Structure Of Hla-Dr4 Complexed With A Peptide From Human Collagen Ii
 >gi|2780937|pdb|5TSS|B Chain B, Toxic Shock Syndrome Toxin-1: Orthorhombic P222(1) Crystal Form
 >gi|2780936|pdb|5TSS|A Chain A, Toxic Shock Syndrome Toxin-1: Orthorhombic P222(1) Crystal Form
 >gi|2780930|pdb|4TSS| Toxic Shock Syndrome Toxin-1: Tetragonal P4(1)2(1)2 Crystal Form
 >gi|2780925|pdb|3TSS| Toxic Shock Syndrome Toxin-1 Tetramutant, P2(1) Crystal Form
 >gi|2780919|pdb|2TSS|C Chain C, Toxic Shock Syndrome Toxin-1 From Staphylococcus Aureus: Orthorhombic P222(1) Crystal Form
 >gi|2780918|pdb|2TSS|B Chain B, Toxic Shock Syndrome Toxin-1 From Staphylococcus Aureus: Orthorhombic P222(1) Crystal Form
 >gi|2780917|pdb|2TSS|A Chain A, Toxic Shock Syndrome Toxin-1 From Staphylococcus Aureus: Orthorhombic P222(1) Crystal Form
 >gi|2392714|pdb|2QIL|C Chain C, Toxic Shock Syndrome Toxin-1 At 2.07 A Resolution
 >gi|2392713|pdb|2QIL|B Chain B, Toxic Shock Syndrome Toxin-1 At 2.07 A Resolution
 >gi|2392712|pdb|2QIL|A Chain A, Toxic Shock Syndrome Toxin-1 At 2.07 A Resolution
 >gi|1310952|pdb|2SOB| Sn-Ob, Ob-Fold Sub-Domain Of Staphylococcal Nuclease, Nmr, 10 Structures
 >gi|2781288|pdb|1SXT|B Chain B, Staphylococcal Enterotoxin Type A (Sea) Co-Crystallised With Zinc
 >gi|2781287|pdb|1SXT|A Chain A, Staphylococcal Enterotoxin Type A (Sea) Co-Crystallised With Zinc
 >gi|2624726|pdb|1SE4| Staphylococcal Enterotoxin B Complexed With Lactose
 >gi|2392546|pdb|1SE3| Staphylococcal Enterotoxin B Complexed With Gm3 Trisaccharide

>gi|2098291|pdb|1SND|B Chain B, Staphylococcal Nuclease Dimer Containing A Deletion Of Residues 114-119 Complexed With Calcium Chloride And The Competitive Inhibitor Deoxythymidine-3',5'-Diphosphate
>gi|2098290|pdb|1SND|A Chain A, Staphylococcal Nuclease Dimer Containing A Deletion Of Residues 114-119 Complexed With Calcium Chloride And The Competitive Inhibitor Deoxythymidine-3',5'-Diphosphate
>gi|1942753|pdb|1STE| Staphylococcal Enterotoxin C2 From Staphylococcus Aureus
>gi|1633348|pdb|1SEB|H Chain H, Complex Of The Human Mhc Class Ii Glycoprotein Hla-Dr1 And The Bacterial Superantigen Seb
>gi|1633344|pdb|1SEB|D Chain D, Complex Of The Human Mhc Class Ii Glycoprotein Hla-Dr1 And The Bacterial Superantigen Seb
>gi|1431724|pdb|1SE2| Staphylococcal Enterotoxin C2, Monoclinic Form
>gi|3212584|pdb|1OME|B Chain B, Crystal Structure Of The Omega Loop Deletion Mutant (Residues 163 - 178 Deleted) Of Beta-Lactamase From Staphylococcus Aureus Pcl
>gi|3212583|pdb|1OME|A Chain A, Crystal Structure Of The Omega Loop Deletion Mutant (Residues 163 - 178 Deleted) Of Beta-Lactamase From Staphylococcus Aureus Pcl
>gi|2392515|pdb|1QIL|C Chain C, Inactive Mutant Toxic Shock Syndrome Toxin-1 At 2.5 A
>gi|2392514|pdb|1QIL|B Chain B, Inactive Mutant Toxic Shock Syndrome Toxin-1 At 2.5 A
>gi|2392513|pdb|1QIL|A Chain A, Inactive Mutant Toxic Shock Syndrome Toxin-1 At 2.5 A
>gi|2392479|pdb|1NUC| Staphylococcal Nuclease, V23c Variant
>gi|2624537|pdb|1JCK|D Chain D, T-Cell Receptor Beta Chain Complexed With Sec3 Superantigen
>gi|2624535|pdb|1JCK|B Chain B, T-Cell Receptor Beta Chain Complexed With Sec3 Superantigen
>gi|2098496|pdb|1KGE| Structure Of Beta-Lactamase Asn 170 Met Mutant
>gi|1942204|pdb|1KGF| Structure Of Beta-Lactamase Asn 170 Gln Mutant
>gi|1827772|pdb|1KNY|B Chain B, Kanamycin Nucleotidyltransferase
>gi|1827771|pdb|1KNY|A Chain A, Kanamycin Nucleotidyltransferase
>gi|2982092|pdb|1EXF|A Chain A, Exfoliative Toxin A
>gi|2098519|pdb|1EDL| Staphylococcal Protein A E-Domain (-60), Nmr, 22 Structures
>gi|2098517|pdb|1EDI| Staphylococcal Protein A E-Domain (180), Nmr, Minimized Average Structure
>gi|2098516|pdb|1EDJ| Staphylococcal Protein A E-Domain (180), Nmr, 20 Structures
>gi|2098515|pdb|1EDK| Staphylococcal Protein A E-Domain (-60), Nmr, Minimized Average Structure
>gi|1942144|pdb|1DJC| Structure Of Beta-Lactamase Precursor, S70a Mutant, At 120k
>gi|1942143|pdb|1DJB| Structure Of Beta-Lactamase Precursor, S70a Mutant, At 298k
>gi|1942142|pdb|1DJA| Structure Of Beta-Lactamase Precursor, K73h Mutant, At 298k
>gi|1633233|pdb|1ESF|B Chain B, Staphylococcal Enterotoxin A
>gi|1633232|pdb|1ESF|A Chain A, Staphylococcal Enterotoxin A
>gi|1942696|pdb|1BDD| Staphylococcus Aureus Protein A, Immunoglobulin-Binding B Domain, Nmr, Minimized Average Structure
>gi|1942695|pdb|1BDC| Staphylococcus Aureus Protein A, Immunoglobulin-Binding B Domain, Nmr, 10 Structures
>gi|3318765|pdb|1AMX| Collagen-Binding Domain From A Staphylococcus Aureus Adhesin
>gi|3212427|pdb|1AD4|B Chain B, Dihydropteroate Synthetase Complexed With Oh-Ch2-Pterin-Pyrophosphate From Staphylococcus Aureus
>gi|3212426|pdb|1AD4|A Chain A, Dihydropteroate Synthetase Complexed With Oh-Ch2-Pterin-Pyrophosphate From Staphylococcus Aureus
>gi|3212425|pdb|1AD1|B Chain B, Dihydropteroate Synthetase (Apo Form) From Staphylococcus Aureus
>gi|3212424|pdb|1AD1|A Chain A, Dihydropteroate Synthetase (Apo Form) From Staphylococcus Aureus
>gi|2554719|pdb|1AGJ|B Chain B, Epidermolytic Toxin A From Staphylococcus Aureus
>gi|2554718|pdb|1AGJ|A Chain A, Epidermolytic Toxin A From Staphylococcus Aureus
>gi|2554635|pdb|1ALQ| Circularly Permuted Beta-Lactamase From Staphylococcus Aureus Pcl
>gi|2392077|pdb|1AEX| Staphylococcal Nuclease, Methane Thiol Disulfide To V23c Variant
>gi|3212327|pdb|1A3V| Staphylococcal Nuclease, Cyclopentane Thiol Disulfide To V23c Variant
>gi|3212326|pdb|1A3U| Staphylococcal Nuclease, Cyclohexane Thiol Disulfide To V23c Variant
>gi|3212325|pdb|1A3T| Staphylococcal Nuclease, V23c Variant, Complex With 2-Fluoroethane Thiol And 3',5'-Thymidine Diphosphate
>gi|3212274|pdb|1A2U| Staphylococcal Nuclease, V23c Variant, Complex With 1-N-Butane Thiol And 3',5'-Thymidine Diphosphate
>gi|3212273|pdb|1A2T| Staphylococcal Nuclease, B-Mercaptoethanol Disulfide To V23c Variant
>gi|3776113|emb|CAA11406.1| succinate dehydrogenase complex, cytochrome b558 subunit [Staphylococcus aureus]
>gi|3776112|emb|CAA11405.1| excinuclease ABC, subunit C [Staphylococcus aureus]
>gi|3776111|emb|CAA11404.1| thioredoxin [Staphylococcus aureus]
>gi|3776110|emb|CAA11403.1| Muts-like protein [Staphylococcus aureus]
>gi|3747042|gb|AAC64162.1| tyrosine recombinase XerD [Staphylococcus aureus]
>gi|3676411|gb|AAC63227.1| putative transposase TnpE [Staphylococcus aureus]
>gi|3676410|gb|AAC63226.1| thymidylate synthetase ThyE [Staphylococcus aureus]
>gi|3676409|gb|AAC63225.1| trimethoprim resistance protein DfrA [Staphylococcus aureus]
>gi|3676408|gb|AAC63224.1| unknown [Staphylococcus aureus]
>gi|3676407|gb|AAC63223.1| putative transposase TnpD [Staphylococcus aureus]
>gi|3676406|gb|AAC63222.1| replication protein Rep [Staphylococcus aureus]
>gi|3676405|gb|AAC63221.1| putative transposase TnpC [Staphylococcus aureus]
>gi|3676456|gb|AAC61974.1| putative transposase TnpG [Staphylococcus aureus]
>gi|3676455|gb|AAC61973.1| putative transposase TnpF [Staphylococcus aureus]

>gi|3676454|gb|AAC61972.1| bifunctional aminoglycoside modifying enzyme AacA-AphD [Staphylococcus aureus]
 >gi|3676453|gb|AAC61971.1| unknown [Staphylococcus aureus]
 >gi|3676452|gb|AAC61970.1| putative transposase TnpE [Staphylococcus aureus]
 >gi|3676451|gb|AAC61969.1| multidrug resistance efflux protein Smr [Staphylococcus aureus]
 >gi|3676450|gb|AAC61968.1| putative replication initiation protein Rep(RC) [Staphylococcus aureus]
 >gi|3676449|gb|AAC61967.1| putative transposase TnpD [Staphylococcus aureus]
 >gi|3676448|gb|AAC61966.1| unknown [Staphylococcus aureus]
 >gi|3676447|gb|AAC61965.1| putative single-stranded DNA binding protein TraM [Staphylococcus aureus]
 >gi|3676446|gb|AAC61964.1| putative membrane protein TraL [Staphylococcus aureus]
 >gi|3676445|gb|AAC61963.1| putative membrane protein TraK [Staphylococcus aureus]
 >gi|3676444|gb|AAC61962.1| putative membrane protein TraJ [Staphylococcus aureus]
 >gi|3676443|gb|AAC61961.1| putative topoisomerase TraI [Staphylococcus aureus]
 >gi|3676442|gb|AAC61960.1| lipoprotein TraH [Staphylococcus aureus]
 >gi|3676441|gb|AAC61959.1| putative membrane protein TraG [Staphylococcus aureus]
 >gi|3676440|gb|AAC61958.1| putative membrane protein TraF [Staphylococcus aureus]
 >gi|3676439|gb|AAC61957.1| putative ATPase TraE [Staphylococcus aureus]
 >gi|3676438|gb|AAC61956.1| TraD [Staphylococcus aureus]
 >gi|3676437|gb|AAC61955.1| putative membrane protein TraC [Staphylococcus aureus]
 >gi|3676436|gb|AAC61954.1| putative membrane protein TraB [Staphylococcus aureus]
 >gi|3676435|gb|AAC61953.1| TraA [Staphylococcus aureus]
 >gi|3676434|gb|AAC61952.1| putative regulator of transfer genes ArtA [Staphylococcus aureus]
 >gi|3676433|gb|AAC61951.1| putative transposase TnpC [Staphylococcus aureus]
 >gi|3676432|gb|AAC61950.1| aminoglycoside adenylyltransferase AadD [Staphylococcus aureus]
 >gi|3676431|gb|AAC61949.1| bleomycin resistance protein Ble [Staphylococcus aureus]
 >gi|3676430|gb|AAC61948.1| Pre [Staphylococcus aureus]
 >gi|3676429|gb|AAC61947.1| putative transposase TnpB [Staphylococcus aureus]
 >gi|3676428|gb|AAC61946.1| membrane protein [Staphylococcus aureus]
 >gi|3676427|gb|AAC61945.1| putative transposase TnpA [Staphylococcus aureus]
 >gi|3676426|gb|AAC61944.1| putative replication initiation protein Rep [Staphylococcus aureus]
 >gi|3676425|gb|AAC61943.1| unknown [Staphylococcus aureus]
 >gi|3676424|gb|AAC61942.1| unknown [Staphylococcus aureus]
 >gi|3676423|gb|AAC61941.1| unknown [Staphylococcus aureus]
 >gi|3676422|gb|AAC61940.1| putative membrane protein [Staphylococcus aureus]
 >gi|3676421|gb|AAC61939.1| unknown [Staphylococcus aureus]
 >gi|3676420|gb|AAC61938.1| oriT nickase Nes [Staphylococcus aureus]
 >gi|3676419|gb|AAC61937.1| LtrC-like protein [Staphylococcus aureus]
 >gi|3676418|gb|AAC61936.1| unknown [Staphylococcus aureus]
 >gi|3676417|gb|AAC61935.1| unknown [Staphylococcus aureus]
 >gi|3676416|gb|AAC61934.1| putative resolvase Res [Staphylococcus aureus]
 >gi|3676415|gb|AAC61933.1| unknown [Staphylococcus aureus]
 >gi|3676414|gb|AAC61932.1| unknown [Staphylococcus aureus]
 >gi|3676413|gb|AAC61931.1| unknown [Staphylococcus aureus]
 >gi|410007|gb|AAC60446.1| leukocidin F component [Staphylococcus aureus, MRSA No. 4, Peptide, 323 aa]
 >gi|410006|gb|AAC60445.1| leukocidin S component [Staphylococcus aureus, MRSA No. 4, Peptide, 315 aa]
 >gi|410005|gb|AAC60444.1| gamma-hemolysin II, H gamma II [Staphylococcus aureus, MRSA No. 4, Peptide, 309 aa]
 >gi|2271510|gb|AAC46291.1| UDP-N-acetylmuramoyl-L-alanine : D-glutamate ligase; MurD [Staphylococcus aureus]
 >gi|1773355|gb|AAC46099.1| Cap5P [Staphylococcus aureus]
 >gi|1773354|gb|AAC46098.1| Cap5O [Staphylococcus aureus]
 >gi|1773353|gb|AAC46097.1| Cap5N [Staphylococcus aureus]
 >gi|1773352|gb|AAC46096.1| Cap5M [Staphylococcus aureus]
 >gi|1773351|gb|AAC46095.1| Cap5L [Staphylococcus aureus]
 >gi|1773350|gb|AAC46094.1| Cap5K [Staphylococcus aureus]
 >gi|1773349|gb|AAC46093.1| Cap5J [Staphylococcus aureus]
 >gi|1773348|gb|AAC46092.1| Cap5I [Staphylococcus aureus]
 >gi|1773347|gb|AAC46091.1| Cap5H [Staphylococcus aureus]
 >gi|1773346|gb|AAC46090.1| Cap5G [Staphylococcus aureus]
 >gi|1773345|gb|AAC46089.1| Cap5F [Staphylococcus aureus]
 >gi|1773344|gb|AAC46088.1| Cap5E [Staphylococcus aureus]
 >gi|1773343|gb|AAC46087.1| Cap5D [Staphylococcus aureus]
 >gi|1773342|gb|AAC46086.1| Cap5C [Staphylococcus aureus]
 >gi|1773341|gb|AAC46085.1| Cap5B [Staphylococcus aureus]
 >gi|1773340|gb|AAC46084.1| Cap5A [Staphylococcus aureus]
 >gi|1673629|gb|AAC46100.1| O-acetyl transferase [Staphylococcus aureus]
 >gi|706922|gb|AAC46354.1| ribosomal protein S7 [Staphylococcus aureus]
 >gi|706921|gb|AAC46353.1| ribosomal protein S12 [Staphylococcus aureus]
 >gi|706920|gb|AAC46352.1| unknown [Staphylococcus aureus]

>gi|2589184|gb|AAC45836.1|GSA-1-aminotransferase [Staphylococcus aureus]
>gi|2589183|gb|AAC45835.1|d-aminolevulinic acid dehydratase [Staphylococcus aureus]
>gi|2589182|gb|AAC45834.1|uroporphyrinogen III synthase [Staphylococcus aureus]
>gi|2589181|gb|AAC45833.1|porphobilinogen deaminase [Staphylococcus aureus]
>gi|2149898|gb|AAC45629.1|cell division protein [Staphylococcus aureus]
>gi|2149897|gb|AAC45628.1|cell division protein [Staphylococcus aureus]
>gi|2149896|gb|AAC45627.1|cell division protein [Staphylococcus aureus]
>gi|2149895|gb|AAC45626.1|D-glutamic acid adding enzyme [Staphylococcus aureus]
>gi|2149894|gb|AAC45625.1|phospho-N-muramic acid-pentapeptide translocase [Staphylococcus aureus]
>gi|2149893|gb|AAC45624.1|penicillin-binding protein 1 [Staphylococcus aureus]
>gi|2149892|gb|AAC45623.1|cell division protein [Staphylococcus aureus]
>gi|2149891|gb|AAC45622.1|unknown [Staphylococcus aureus]
>gi|2149890|gb|AAC45621.1|unknown [Staphylococcus aureus]
>gi|1314302|gb|AAC45357.1|isoleucyl-tRNA synthetase [Staphylococcus aureus]
>gi|1314301|gb|AAC45356.1|unknown [Staphylococcus aureus]
>gi|1575026|gb|AAC44840.1|LrgB
>gi|1575025|gb|AAC44839.1|holin-like protein LrgA
>gi|710422|gb|AAC44803.1|cmp-binding-factor 1
>gi|710421|gb|AAC44802.1|unknown
>gi|1595810|gb|AAC44435.1|type-I signal peptidase SpsB [Staphylococcus aureus]
>gi|1595809|gb|AAC44434.1|type-I signal peptidase SpsA [Staphylococcus aureus]
>gi|1397239|gb|AAC44135.1|elastin binding protein
>gi|1001961|gb|AAC43470.1|MHC class II analog
>gi|3327949|gb|AAC38785.1|putative recombinase Sin [Staphylococcus aureus]
>gi|3327948|gb|AAC38784.1|multidrug efflux protein QacB [Staphylococcus aureus]
>gi|3327947|gb|AAC38783.1|transcriptional regulator QacR [Staphylococcus aureus]
>gi|3327945|gb|AAC38782.1|putative transposase TnpA [Staphylococcus aureus]
>gi|3327944|gb|AAC38781.1|delta-orf186 [Staphylococcus aureus]
>gi|3327943|gb|AAC38780.1|multidrug efflux protein QacB [Staphylococcus aureus]
>gi|3327942|gb|AAC38779.1|transcriptional regulator QacR [Staphylococcus aureus]
>gi|3135292|gb|AAC38560.1|large conductance mechanosensitive channel [Staphylococcus aureus]
>gi|2827912|gb|AAC38446.1|IgG-binding protein SBI [Staphylococcus aureus]
>gi|2565311|gb|AAC38087.1|high affinity proline permease [Staphylococcus aureus]
>gi|2315995|gb|AAC38146.1|branched-chain amino acid carrier protein [Staphylococcus aureus]
>gi|4379428|emb|CAA11546.1|thioredoxin reductase [Staphylococcus aureus]
>gi|3445567|gb|AAC32485.1|transport protein [Staphylococcus aureus]
>gi|3445566|gb|AAC32484.1|repressor protein [Staphylococcus aureus]
>gi|3411114|gb|AAC31156.1|DNA topoisomerase IV subunit A [Staphylococcus aureus]
>gi|3411112|gb|AAC31155.1|DNA topoisomerase IV subunit A [Staphylococcus aureus]
>gi|3411110|gb|AAC31154.1|DNA topoisomerase IV subunit A [Staphylococcus aureus]
>gi|3411108|gb|AAC31153.1|DNA topoisomerase IV subunit A [Staphylococcus aureus]
>gi|3411106|gb|AAC31152.1|DNA topoisomerase IV subunit A [Staphylococcus aureus]
>gi|3411104|gb|AAC31151.1|DNA topoisomerase IV subunit A [Staphylococcus aureus]
>gi|3411102|gb|AAC31150.1|DNA topoisomerase IV subunit A [Staphylococcus aureus]
>gi|3411100|gb|AAC31149.1|DNA topoisomerase IV subunit A [Staphylococcus aureus]
>gi|3411098|gb|AAC31148.1|DNA topoisomerase IV subunit A [Staphylococcus aureus]
>gi|3411096|gb|AAC31147.1|DNA topoisomerase IV subunit A [Staphylococcus aureus]
>gi|3411092|gb|AAC31144.1|DNA gyrase subunit A; topoisomerase [Staphylococcus aureus]
>gi|3411090|gb|AAC31143.1|DNA gyrase subunit A; topoisomerase [Staphylococcus aureus]
>gi|3411088|gb|AAC31142.1|DNA gyrase subunit A; topoisomerase [Staphylococcus aureus]
>gi|3411086|gb|AAC31141.1|DNA gyrase subunit A; topoisomerase [Staphylococcus aureus]
>gi|3411084|gb|AAC31140.1|DNA gyrase subunit A; topoisomerase [Staphylococcus aureus]
>gi|3411082|gb|AAC31139.1|DNA gyrase subunit A; topoisomerase [Staphylococcus aureus]
>gi|3411080|gb|AAC31138.1|DNA gyrase subunit A; topoisomerase [Staphylococcus aureus]
>gi|3411078|gb|AAC31137.1|DNA gyrase subunit A; topoisomerase [Staphylococcus aureus]
>gi|3411076|gb|AAC31136.1|DNA gyrase subunit A; topoisomerase [Staphylococcus aureus]
>gi|3411074|gb|AAC31135.1|DNA gyrase subunit A; topoisomerase [Staphylococcus aureus]
>gi|2689564|gb|AAC28969.1|integrase [Staphylococcus aureus]
>gi|2689563|gb|AAC28968.1|enterotoxin [Staphylococcus aureus]
>gi|2689562|gb|AAC28967.1|orf15 [Staphylococcus aureus]
>gi|2689561|gb|AAC28966.1|orf14 [Staphylococcus aureus]
>gi|2689560|gb|AAC28965.1|orf13 [Staphylococcus aureus]
>gi|2689559|gb|AAC28964.1|orf12 [Staphylococcus aureus]
>gi|2689558|gb|AAC28963.1|orf11 [Staphylococcus aureus]
>gi|2689557|gb|AAC28962.1|orf10 [Staphylococcus aureus]
>gi|2689556|gb|AAC28961.1|orf9 [Staphylococcus aureus]
>gi|2689555|gb|AAC28960.1|orf8 [Staphylococcus aureus]
>gi|2689554|gb|AAC28959.1|orf7 [Staphylococcus aureus]
>gi|2689553|gb|AAC28958.1|orf6 [Staphylococcus aureus]
>gi|2689552|gb|AAC28957.1|orf5 [Staphylococcus aureus]
>gi|2689551|gb|AAC28956.1|orf4 [Staphylococcus aureus]

>gi|2689550|gb|AAC28955.1| orf3 [Staphylococcus aureus]
>gi|2689549|gb|AAC28954.1| toxic shock syndrome toxin-1 [Staphylococcus aureus]
>gi|2689548|gb|AAC28953.1| orf1 [Staphylococcus aureus]
>gi|3393011|emb|CAA12115.1| Clumping factor B [Staphylococcus aureus]
>gi|3323613|gb|AAC26661.1| extracellular enterotoxin type I precursor [Staphylococcus aureus]
>gi|3323611|gb|AAC26660.1| extracellular enterotoxin type G precursor [Staphylococcus aureus]
>gi|3256224|emb|CAA74741.1| ypfP [Staphylococcus aureus]
>gi|3256223|emb|CAA74740.1| UDP-N-acetylmuramyl-tripeptide synthetase [Staphylococcus aureus]
>gi|3256222|emb|CAA74739.1| peptide chain release factor 3 [Staphylococcus aureus]
>gi|230814|pdb|3BLM| Beta-Lactamase (E.C.3.5.2.6)
>gi|230746|pdb|2SNS| Staphylococcal Nuclease (E.C.3.1.33.1) Complex With 2(Prime)-Deoxy-3(Prime)-5(Prime)-Diphosphothymidine
>gi|230745|pdb|2SNM| Staphylococcal Nuclease (E.C.3.1.31.1) Mutant With Val 66 Replaced By Lys (V66k)
>gi|576398|pdb|2ENB| Staphylococcal Nuclease (E.C.3.1.31.1) Mutation With Asp 21 Replaced By Glu (D21e) Complexed With The Inhibitor Thymidine 3',5'-Diphosphate
>gi|443374|pdb|2DTB| Delta-Toxin (Delta-Haemolysin) (Nmr, 9 Structures)
>gi|1421454|pdb|1ZER| Mol_id: 1; Molecule: Histidine-Containing Phosphocarrier Protein; Chain: Null; Synonym: Hpr
>gi|576294|pdb|1SYG| Staphylococcal Nuclease (E.C.3.1.31.1) Mutant With Pro 117 Replaced By Ala (P117a)
>gi|576293|pdb|1SYF| Staphylococcal Nuclease (E.C.3.1.31.1) Mutant With Pro 117 Replaced By Thr (P117t) Complexed With 2'-Deoxy-3'-5'-Diphosphothymidine And Calcium
>gi|576292|pdb|1SYE| Staphylococcal Nuclease (E.C.3.1.31.1) Mutant With Pro 117 Replaced By Thr (P117t)
>gi|576291|pdb|1SYD| Staphylococcal Nuclease (E.C.3.1.31.1) Mutant With Pro 117 Replaced By Gly (P117g) Complexed With 2'-Deoxy-3'-5'-Diphosphothymidine And Calcium
>gi|576290|pdb|1SYC| Staphylococcal Nuclease (E.C.3.1.31.1) Mutant With Pro 117 Replaced By Gly (P117g)
>gi|576289|pdb|1SYB| Staphylococcal Nuclease (E.C.3.1.31.1) With Residues 27 - 31 (Tyr-Lys-Gly-Gln-Pro) Replaced With Residues 160 - 165 Of Concanavalin A (Ser-Ser-Asn-Gly-Ser-Pro) Complexed With 2'-Deoxy-3'-5'-Diphosphothymidine And Calcium
>gi|349914|pdb|1STY| Staphylococcal Nuclease (E.C.3.1.31.1) Insertion Mutant With Glycine Residue Inserted In An Alpha Helix, Between Arg126 And Lys127 (126g127) Complex With Calcium And Inhibitor Thymidine 3',5'-Bisphosphate
>gi|999674|pdb|1STH| Staphylococcal Nuclease (E.C.3.1.31.1) Complexed With Co(Ii) Ion And Thymidine 3',5'-Bisphosphate (Pdtp)
>gi|999672|pdb|1STG| Staphylococcal Nuclease (E.C.3.1.31.1)
>gi|576287|pdb|1STN| Staphylococcal Nuclease (E.C.3.1.31.1)
>gi|576286|pdb|1STB| Staphylococcal Nuclease (E.C.3.1.31.1) Insertion Mutant With Leu Inserted At The End Of The Third Beta-Strand Between Leu 36 And Leu 37 (Ins(L36-L)) Complexed With Thymidine 3',5'-Diphosphate And Calcium
>gi|576285|pdb|1STA| Staphylococcal Nuclease (E.C.3.1.31.1) Double Insertion Mutant With Two Glycine Residues Inserted In The First Beta Strand Between Pro 11 And Ala 12 (Ins(P11-Gg)) Complexed With Calcium And The Inhibitor Thymidine 3',5'-Diphosphate
>gi|230332|pdb|1SNM| Staphylococcal Nuclease (E.C.3.1.31.1) Mutant (Glu 43 Replaced By Asp) (E43D) Complex With A Calcium Ion And 3-Prime, 5-Prime-Deoxythymidine Bisphosphate
>gi|230331|pdb|1SNC| Staphylococcal Nuclease (E.C.3.1.31.1) Complex With A Calcium Ion And 3-Prime, 5-Prime-Deoxythymidine Bisphosphate
>gi|1431686|pdb|1PIO|B Chain B, Mol_id: 1; Molecule: Beta-Lactamase; Chain: A, B; Synonym: Penicillinase; Ec: 3.5.2.6; Engineered: Yes; Mutation: Ins(Met 30), A238s, Del(I239)
>gi|1431685|pdb|1PIO|A Chain A, Mol_id: 1; Molecule: Beta-Lactamase; Chain: A, B; Synonym: Penicillinase; Ec: 3.5.2.6; Engineered: Yes; Mutation: Ins(Met 30), A238s, Del(I239)
>gi|1127093|pdb|1NSN|S Chain S, Immunoglobulin, Staphylococcal Nuclease Mol_id: 1; Molecule: Igg Fab (Igg1, Kappa); Chain: L, H; Domain: Fragment N10; Synonym: N10 Fab Immunoglobulin; Mol_id: 2; Molecule: Staphylococcal Nuclease; Chain: S; Synonym: Staphylococcal Nuclease Ribonucleate, (Deoxyribonucleate)-3'-Nucleotidohydrolase; Ec: 3.1.31.1; Engineered: Yes
>gi|999581|pdb|1KDC| Staphylococcal Nuclease (E.C.3.1.31.1) Mutant With Lys 116 Replaced By Asn (K116n)
>gi|999578|pdb|1KDB| Staphylococcal Nuclease (E.C.3.1.31.1) Mutant With Lys 116 Replaced By Glu (K116e)
>gi|999577|pdb|1KDA| Staphylococcal Nuclease (E.C.3.1.31.1) Mutant With Lys 116 Replaced By Asp (K116d)
>gi|640137|pdb|1KAN|B Chain B, Kanamycin Nucleotidyltransferase (E.C.2.7.7.-) Mutant With Asp 80 Replaced By Tyr And Thr 130 Replaced By Lys (D80y,T130k)
>gi|640136|pdb|1KAN|A Chain A, Kanamycin Nucleotidyltransferase (E.C.2.7.7.-) Mutant With Asp 80 Replaced By Tyr And Thr 130 Replaced By Lys (D80y,T130k)
>gi|494228|pdb|1KAB| Staphylococcal Nuclease (E.C.3.1.33.1) Mutant With Lys 116 Replaced By Gly (K116g)
>gi|494227|pdb|1KAA| Staphylococcal Nuclease (E.C.3.1.33.1) Mutant With Lys 116 Replaced By Ala (K116a)

>gi|229907|pdb|1FC2|C Chain C, Immunoglobulin Fc And Fragment B Of Protein A Complex
 >gi|576100|pdb|1ENC| Staphylococcal Nuclease (E.C.3.1.31.1) Mutant With Asp 21 Replaced By Glu (D21e) Complexed With A Calcium Ion And The Inhibitor Thymidine 3',5'-Diphosphate
 >gi|576099|pdb|1ENA| Staphylococcal Nuclease (E.C.3.1.31.1) Mutation With Asp 21 Replaced By Glu (D21e) Complexed With A Calcium Ion
 >gi|442844|pdb|1DTC| Acetyl-Delta-Toxin (Acetyl-Delta-Haemolysin) (Nmr, 12 Structures)
 >gi|640251|pdb|1BLH| Beta-Lactamase (E.C.3.5.2.6) Complexed With [(n-(Benzyloxycarbonyl)amino)methyl]phosphonate
 >gi|515092|pdb|1BLP| Beta-Lactamase (E.C.3.5.2.6) P54 Mutant With Asp 179 Replaced By Asn (D179n)
 >gi|493890|pdb|1BLC| Beta-Lactamase (E.C.3.5.2.6) Complex With Degradation Products Of Clavulanate
 >gi|3152725|gb|AAC17130.1| enolase [Staphylococcus aureus]
 >gi|2463563|dbj|BAA22556.1| MURD [Staphylococcus aureus]
 >gi|2463562|dbj|BAA22555.1| MRAY [Staphylococcus aureus]
 >gi|2463561|dbj|BAA22554.1| penicillin-binding protein 1 [Staphylococcus aureus]
 >gi|2463560|dbj|BAA22553.1| unnamed protein product [Staphylococcus aureus]
 >gi|2463559|dbj|BAA22552.1| unnamed protein product [Staphylococcus aureus]
 >gi|1835218|emb|CAA71057.1| seryl-trna synthetase [Staphylococcus aureus]
 >gi|3122772|sp|O31203|RRF1_STAAU PROBABLE RIBOSOME RECYCLING FACTOR (RIBOSOME RELEASING FACTOR) (RRF)
 >gi|1488695|gb|AAC12901.1| novel antigen; orf-2 [Staphylococcus aureus]
 >gi|2826896|dbj|BAA24572.1| RecG [Staphylococcus aureus]
 >gi|2791991|emb|CAA74380.1| putative transposase [Staphylococcus aureus]
 >gi|2791990|emb|CAA74379.1| hypothetical protein [Staphylococcus aureus]
 >gi|2791989|emb|CAA74378.1| hypothetical protein [Staphylococcus aureus]
 >gi|2791988|emb|CAA74377.1| hypothetical protein [Staphylococcus aureus]
 >gi|2791987|emb|CAA74376.1| PBP2A [Staphylococcus aureus]
 >gi|2791986|emb|CAA74375.1| MecR1 protein [Staphylococcus aureus]
 >gi|2791985|emb|CAA74374.1| MecI protein [Staphylococcus aureus]
 >gi|2791984|emb|CAA74373.1| putative repressor [Staphylococcus aureus]
 >gi|2769708|gb|AAB95639.1| pristinamycin resistance protein VgaB [Staphylococcus aureus]
 >gi|2736228|gb|AAB94106.1| transducer protein [Staphylococcus aureus]
 >gi|2736227|gb|AAB94105.1| mutant sensor protein [Staphylococcus aureus]
 >gi|2736226|gb|AAB94104.1| pre-pheromone [Staphylococcus aureus]
 >gi|2736225|gb|AAB94103.1| signal transduction protein [Staphylococcus aureus]
 >gi|2736223|gb|AAB94102.1| transducer protein [Staphylococcus aureus]
 >gi|2736222|gb|AAB94101.1| mutant sensor protein [Staphylococcus aureus]
 >gi|2736221|gb|AAB94100.1| pre-pheromone [Staphylococcus aureus]
 >gi|2736220|gb|AAB94099.1| signal transduction protein [Staphylococcus aureus]
 >gi|2736218|gb|AAB94098.1| transducer protein [Staphylococcus aureus]
 >gi|2736217|gb|AAB94097.1| mutant sensor protein [Staphylococcus aureus]
 >gi|2736216|gb|AAB94096.1| pre-pheromone [Staphylococcus aureus]
 >gi|2736215|gb|AAB94095.1| signal transduction protein [Staphylococcus aureus]
 >gi|2696796|dbj|BAA24012.1| Fmt [Staphylococcus aureus]
 >gi|2696713|dbj|BAA24009.1| integrase [Staphylococcus aureus]
 >gi|2696712|dbj|BAA24008.1| LukF-PV [Staphylococcus aureus]
 >gi|2696711|dbj|BAA24007.1| LukS-PV [Staphylococcus aureus]
 >gi|216977|dbj|BAA00126.1| staphylocoagulase precursor [Staphylococcus aureus]
 >gi|773396|emb|CAA39963.1| QacA protein [Staphylococcus aureus]
 >gi|46660|emb|CAA39962.1| ORF188, has identity with known regulators such as tet regulator in Tn10 [Staphylococcus aureus]
 >gi|2645713|gb|AAB87473.1| ribosome recycling factor [Staphylococcus aureus]
 >gi|2641998|dbj|BAA23610.1| lipophilic protein [Staphylococcus aureus]
 >gi|2580436|dbj|BAA23141.1| histidyl-tRNA synthetase [Staphylococcus aureus]
 >gi|2580435|dbj|BAA23140.1| N-acetylmuramoyl-L-alanine amidase [Staphylococcus aureus]
 >gi|2580434|dbj|BAA23139.1| ORF1 [Staphylococcus aureus]
 >gi|2580433|dbj|BAA23138.1| ppGpp hydrolase [Staphylococcus aureus]
 >gi|2580432|dbj|BAA23137.1| adenine phosphoribosyltransferase [Staphylococcus aureus]
 >gi|1575062|gb|AAB81288.1| lytS [Staphylococcus aureus]
 >gi|1575061|gb|AAB81287.1| ScdA [Staphylococcus aureus]
 >gi|1694677|dbj|BAA13755.1| DnaA [Staphylococcus aureus]
 >gi|2506163|gb|AAB81232.1| AgrD [Staphylococcus aureus]
 >gi|1916240|gb|AAB81231.1| AgrA [Staphylococcus aureus]
 >gi|1916239|gb|AAB81230.1| AgrC-31 [Staphylococcus aureus]
 >gi|1916238|gb|AAB81229.1| AgrB [Staphylococcus aureus]
 >gi|2506165|gb|AAB80783.1| AgrD [Staphylococcus aureus]
 >gi|2506164|gb|AAB80779.1| AgrD [Staphylococcus aureus]
 >gi|1916248|gb|AAB80782.1| AgrA [Staphylococcus aureus]
 >gi|1916247|gb|AAB80781.1| AgrC [Staphylococcus aureus]
 >gi|1916246|gb|AAB80780.1| AgrB [Staphylococcus aureus]
 >gi|1916244|gb|AAB80778.1| AgrA [Staphylococcus aureus]
 >gi|1916243|gb|AAB80777.1| AgrC [Staphylococcus aureus]

>gi|1916316|gb|AAB51151.1| alkyl hydroperoxide reductase subunit C [Staphylococcus aureus]
>gi|1913907|gb|AAB51063.1| TagD [Staphylococcus aureus]
>gi|1913906|gb|AAB51062.1| TagX [Staphylococcus aureus]
>gi|1913905|gb|AAB51061.1| TagB [Staphylococcus aureus]
>gi|1864022|gb|AAB50178.1| penicillin binding protein 4
>gi|881631|gb|AAB50179.1| AbcA
>gi|1657655|gb|AAB49445.1| Cap8P [Staphylococcus aureus]
>gi|1657654|gb|AAB49444.1| Cap8O [Staphylococcus aureus]
>gi|1657653|gb|AAB49443.1| Cap8N [Staphylococcus aureus]
>gi|1657652|gb|AAB49442.1| Cap8M [Staphylococcus aureus]
>gi|1657651|gb|AAB49441.1| Cap8L [Staphylococcus aureus]
>gi|1657650|gb|AAB49440.1| Cap8K [Staphylococcus aureus]
>gi|1657649|gb|AAB49439.1| Cap8J [Staphylococcus aureus]
>gi|1657648|gb|AAB49438.1| Cap8I [Staphylococcus aureus]
>gi|1657647|gb|AAB49437.1| Cap8H [Staphylococcus aureus]
>gi|1657646|gb|AAB49436.1| Cap8G [Staphylococcus aureus]
>gi|1657645|gb|AAB49435.1| Cap8F [Staphylococcus aureus]
>gi|1657644|gb|AAB49434.1| Cap8E [Staphylococcus aureus]
>gi|1657643|gb|AAB49433.1| Cap8D [Staphylococcus aureus]
>gi|1657642|gb|AAB49432.1| Cap8C [Staphylococcus aureus]
>gi|1657641|gb|AAB49431.1| Cap8B [Staphylococcus aureus]
>gi|1657640|gb|AAB49430.1| Cap8A [Staphylococcus aureus]
>gi|1854577|gb|AAB48183.1| lytR [Staphylococcus aureus]
>gi|862312|gb|AAB48182.1| lytS [Staphylococcus aureus]
>gi|1731452|gb|AAB48104.1| recombination protein [Staphylococcus aureus]
>gi|1053003|gb|AAB48103.1| CAT protein [Staphylococcus aureus]
>gi|1053002|gb|AAB48102.1| replication protein [Staphylococcus aureus]
>gi|1848269|gb|AAB47993.1| quaternary ammonium compounds resistance protein Qac [Staphylococcus aureus]
>gi|1848268|gb|AAB47992.1| replication protein Rep [Staphylococcus aureus]
>gi|677847|emb|CAA24593.1| reading frame A [Staphylococcus aureus]
>gi|677846|emb|CAA24590.1| reading frame C [Staphylococcus aureus]
>gi|677845|emb|CAA24589.1| reading frame D [Staphylococcus aureus]
>gi|677844|emb|CAA24588.1| reading frame E [Staphylococcus aureus]
>gi|46746|emb|CAA38969.1| truncated alpha-toxin [Staphylococcus aureus]
>gi|46559|emb|CAA24592.1| reading frame F transl. attenuator [Staphylococcus aureus]
>gi|46558|emb|CAA24591.1| reading frame B mls resistance [Staphylococcus aureus]
>gi|987499|gb|AAB41908.1| 5-dehydroquinase synthase
>gi|987498|gb|AAB41907.1| chorismate synthase
>gi|987497|gb|AAB41906.1| nucleoside diphosphate kinase
>gi|987496|gb|AAB41905.1| geranylgeranyl pyrophosphate synthetase homolog; Method: conceptual translation supplied by author
>gi|1262138|emb|CAA62900.1| glycerol 3-phosphate cytidyltransferase [Staphylococcus aureus]
>gi|1262137|emb|CAA62899.1| penicillin-binding protein 4 [Staphylococcus aureus]
>gi|1262136|emb|CAA62898.1| ATP-binding cassette transporter A [Staphylococcus aureus]
>gi|1045529|gb|AAB39957.1| beta-lactamase
>gi|1045527|gb|AAB39956.1| beta-lactamase
>gi|1045525|gb|AAB39955.1| tetracycline resistance protein [Staphylococcus aureus]
>gi|1045524|gb|AAB39954.1| replication protein [Staphylococcus aureus]
>gi|1684749|emb|CAA70762.1| femD [Staphylococcus aureus]
>gi|1204146|emb|CAA65106.1| fibronectin-binding protein [Staphylococcus aureus]
>gi|1684751|emb|CAA70579.1| DNA directed RNA polymerase beta' chain [Staphylococcus aureus]
>gi|1478385|gb|AAB36169.1| MsrSa=63 kda MsrA homolog {N-terminal} [Staphylococcus aureus, clinical isolate, pEP2104, Peptide Plasmid Partial, 31 aa]
>gi|1042046|gb|AAB34958.1| IgG-binding polypeptide=protein A homolog [Staphylococcus aureus, strain 8325-4, Peptide Partial, 84 aa]
>gi|999313|gb|AAB34910.1| 60 kda vitronectin-binding surface protein {N-terminal} [Staphylococcus aureus, prototype V8, Peptide Partial, 20 aa]
>gi|998765|gb|AAB34258.1| enterotoxin H {N-terminal} [Staphylococcus aureus, FRI-569, Peptide Partial, 30 aa]
>gi|894289|gb|AAB33482.1| alkaline shock protein 23, ASP23 [Staphylococcus aureus, 912, Peptide, 169 aa]
>gi|619317|gb|AAB32218.1| beta-hemolysin, phospholipase C, PLC [Staphylococcus aureus, 126/89, Peptide, 331 aa]
>gi|693735|gb|AAB31949.1| NorA {ISP794, quinolone resistance} [Staphylococcus aureus, NCTC 8325, Peptide Insertion, 388 aa]
>gi|456770|gb|AAB28795.1| Tet(K)=tetracycline efflux protein [Staphylococcus aureus, pT181, Peptide Plasmid, 459 aa]
>gi|433036|gb|AAB28599.1| adhesin {collagen binding domain} [Staphylococcus aureus, FDA 574, Peptide Partial, 37 aa]
>gi|1680566|gb|AH004229.1| No definition line found

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>gi|1680565|gb|AH004228.1| No definition line found
>gi|299115|gb|AAB26122.1| gamma-hemolysin component II, H gamma II=leukocidin S homolog
[Staphylococcus aureus, 4, RIMD 310925, Peptide Partial, 5 aa, segment 2 of 2]
>gi|299114|gb|AAB26121.1| gamma-hemolysin component II, H gamma II=leukocidin S homolog
[Staphylococcus aureus, 4, RIMD 310925, Peptide Partial, 58 aa, segment 1 of 2]
>gi|299112|gb|AAB26120.1| gamma-hemolysin component I, H gamma I=leukocidin F homolog
[Staphylococcus aureus, 4, RIMD 310925, Peptide Partial, 2 aa, segment 2 of 2]
>gi|299111|gb|AAB26119.1| gamma-hemolysin component I, H gamma I=leukocidin F homolog
[Staphylococcus aureus, 4, RIMD 310925, Peptide Partial, 59 aa, segment 1 of 2]
>gi|265412|gb|AAB25337.1| V8 protease [Staphylococcus aureus, Peptide, 276 aa]
>gi|248665|gb|AAB22051.1| chloramphenicol acetyltransferase, CAT [EC 2.3.1.28] [Staphylococcus aureus, 4.6 kb chloramphenicol resistance (CmR) plasmid pSCS6, Peptide Plasmid, 215 aa]
>gi|246440|gb|AAB21603.1| 60 kda cell surface adhesin for heparan sulfate [Staphylococcus aureus, Peptide Partial, 4 aa]
>gi|246439|gb|AAB21602.1| 66 kda cell surface adhesin for heparan sulfate [Staphylococcus aureus, Peptide Partial, 9 aa]
>gi|239960|gb|AAB20545.1| 25-kda elastin-binding protein [Staphylococcus aureus, Peptide Partial, 14 aa]
>gi|239959|gb|AAB20544.1| 40-kda elastin-binding protein [Staphylococcus aureus, Peptide Partial, 18 aa]
>gi|1673527|gb|AAB18959.1| transposase [Staphylococcus aureus]
>gi|1673525|gb|AAB18958.1| transposase [Staphylococcus aureus]
>gi|1644433|gb|AAB17663.1| D-specific D-2-hydroxyacid dehydrogenase [Staphylococcus aureus]
>gi|581567|emb|CAA37260.1| Sau96I DNA methyltransferase [Staphylococcus aureus]
>gi|46618|emb|CAA37259.1| Sau96I restriction endonuclease [Staphylococcus aureus]
>gi|46597|emb|CAA37902.1| transposase [Staphylococcus aureus]
>gi|1587088|prf||2205353A pheromone [Staphylococcus aureus]
>gi|1583755|prf||2121375A MHC class II-like protein [Staphylococcus aureus]
>gi|229342|prf||710414A nuclease [Staphylococcus aureus]
>gi|229233|prf||670719A nuclease [Staphylococcus aureus]
>gi|1096955|prf||2113202C RNA polymerase:SUBUNIT=beta' [Staphylococcus aureus]
>gi|1096954|prf||2113202B RNA polymerase:SUBUNIT=beta [Staphylococcus aureus]
>gi|1096953|prf||2113202A ORF 202 [Staphylococcus aureus]
>gi|1095875|prf||2110238A lipase [Staphylococcus aureus]
>gi|1094971|prf||2107219C RNA polymerase:SUBUNIT=beta' [Staphylococcus aureus]
>gi|1094970|prf||2107219B RNA polymerase:SUBUNIT=beta [Staphylococcus aureus]
>gi|1094969|prf||2107219A rpoB upstream ORF [Staphylococcus aureus]
>gi|1093504|prf||2104216A LukM protein [Staphylococcus aureus]
>gi|1092377|prf||2023311A exotoxin [Staphylococcus aureus]
>gi|742313|prf||2009360B pcrB protein [Staphylococcus aureus]
>gi|742312|prf||2009360A helicase [Staphylococcus aureus]
>gi|448909|prf||1918210C leukocidin [Staphylococcus aureus]
>gi|448908|prf||1918210B leukocidin [Staphylococcus aureus]
>gi|448907|prf||1918210A gamma hemolysin [Staphylococcus aureus]
>gi|444424|prf||1907159A ethidium bromide resistance gene [Staphylococcus aureus]
>gi|384172|prf||1905282A rep protein [Staphylococcus aureus]
>gi|384170|prf||1905280A protein A [Staphylococcus aureus]
>gi|383540|prf||1903261A toxic shock syndrome toxin [Staphylococcus aureus]
>gi|228896|prf||1814271A Glu-C endoprotease [Staphylococcus aureus]
>gi|228567|prf||1806229B repressor [Staphylococcus aureus]
>gi|228566|prf||1806229A coinducer protein [Staphylococcus aureus]
>gi|228100|prf||1717222A REP protein [Staphylococcus aureus]
>gi|227968|prf||1714238A beta lactamase mutant S-3P [Staphylococcus aureus]
>gi|227467|prf||1704203A enterotoxin A [Staphylococcus aureus]
>gi|226860|prf||1609133A plasmid pOX1000 ORF A [Staphylococcus aureus]
>gi|581544|emb|CAA27142.1| kanamycin nucleotidyltransferase (AA 1-253) [Staphylococcus aureus]
>gi|46496|emb|CAA27141.1| repB polypeptide (AA 1-235) [Staphylococcus aureus]
>gi|1245474|gb|AAB09712.1| nicking enzyme [Staphylococcus aureus]
>gi|1586531|prf||2204232B penicillin-binding protein 4 [Staphylococcus aureus]
>gi|1586530|prf||2204232A ABC transporter-like protein [Staphylococcus aureus]
>gi|1585878|prf||2202209C ORF 3 [Staphylococcus aureus]
>gi|1585877|prf||2202209B ORF 2 [Staphylococcus aureus]
>gi|1585876|prf||2202209A ORF 1 [Staphylococcus aureus]
>gi|1053140|gb|AAB09660.1| tetracycline resistance protein [Staphylococcus aureus]
>gi|1575125|gb|AAB09464.1| beta-lactamase
>gi|226340|prf||1507213A transposase, insertion seq IS257 [Staphylococcus aureus]
>gi|225999|prf||1405331D repE gene [Staphylococcus aureus]
>gi|225998|prf||1405331C ORF D [Staphylococcus aureus]
>gi|225997|prf||1405331B rlx gene [Staphylococcus aureus]
>gi|359739|prf||1313299A staphylocoagulase [Staphylococcus aureus]
>gi|225442|prf||1303274B gene B [Staphylococcus aureus]
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>gi|46687|emb|CAA68434.1| preproenzyme (AA -68 to 268) [Staphylococcus aureus]
>gi|1070386|emb|CAA63689.1| phosphoenolpyruvate-protein phosphatase [Staphylococcus aureus]
>gi|1070385|emb|CAA63688.1| histidin-containing protein [Staphylococcus aureus]
>gi|677852|emb|CAA45513.1| DNA-directed RNA polymerase beta' chain [Staphylococcus aureus]
>gi|677851|emb|CAA45512.1| DNA-directed RNA polymerase beta chain [Staphylococcus aureus]
>gi|677850|emb|CAA45511.1| hypothetical protein [Staphylococcus aureus]
>gi|677849|emb|CAA45510.1| ribosomal protein L7/L12 [Staphylococcus aureus]
>gi|581571|emb|CAA43217.1| chlorAMphenicol acetyltransferase [Staphylococcus aureus]
>gi|551670|emb|CAA51251.1| lukS [Staphylococcus aureus]
>gi|551669|emb|CAA51250.1| ORF [Staphylococcus aureus]
>gi|288292|emb|CAA51252.1| leucocidin F [Staphylococcus aureus]
>gi|46652|emb|CAA43218.1| chlorAMphenicol acetyltransferase [Staphylococcus aureus]
>gi|1333818|emb|CAA26369.1| pot. orfB (aa 1-92) (4557 is 2nd base in codon) [Staphylococcus aureus]
>gi|1333817|emb|CAA26368.1| pot. orfA [Staphylococcus aureus]
>gi|809754|emb|CAA26365.1| unidentified reading frame [Staphylococcus aureus]
>gi|581570|emb|CAA41339.1| dihydrolipoamide acetyltransferase: subunit E2 [Staphylococcus aureus]
>gi|581568|emb|CAA27733.1| beta-lactamase (aa 1-281) [Staphylococcus aureus]
>gi|488529|emb|CAA45728.1| S component of leucocodin R [Staphylococcus aureus]
>gi|483534|emb|CAA44177.1| penicillin-binding protein 2 [Staphylococcus aureus]
>gi|295834|emb|CAA39320.1| ORF 154 [Staphylococcus aureus]
>gi|48874|emb|CAA41340.1| dihydrolipoamide dehydrogenase: subunit E3 [Staphylococcus aureus]
>gi|48872|emb|CAA41338.1| pyruvate dehydrogenase (lipoamide): subunit E1beta [Staphylococcus aureus]
>gi|46647|emb|CAA29842.1| ORF (repE) [Staphylococcus aureus]
>gi|46646|emb|CAA29841.1| orfD [Staphylococcus aureus]
>gi|46645|emb|CAA29840.1| ORF (rlx) [Staphylococcus aureus]
>gi|46644|emb|CAA29839.1| ORF (str) [Staphylococcus aureus]
>gi|46639|emb|CAA31314.1| ORF 1 (AA 1 - 330) [Staphylococcus aureus]
>gi|46638|emb|CAA31313.1| ORF 2 (AA 1 - 236) [Staphylococcus aureus]
>gi|46636|emb|CAA30291.1| RepM protein (AA 1 - 314) [Staphylococcus aureus]
>gi|46632|emb|CAA26367.1| CAT gene (aa 1-215) [Staphylococcus aureus]
>gi|46631|emb|CAA26366.1| repD (aa 1-311) [Staphylococcus aureus]
>gi|46629|emb|CAA68684.1| penicillin-binding protein (AA 1-670) [Staphylococcus aureus]
>gi|46622|emb|CAA42079.1| E.coli isoleucyl tRNA synthetase homologue [Staphylococcus aureus]
>gi|46620|emb|CAA42080.1| E.coli isoleucyl tRNA synthetase homologue [Staphylococcus aureus]
>gi|46611|emb|CAA36829.1| PBP2' (AA 1-668) [Staphylococcus aureus]
>gi|46609|emb|CAA45729.1| F component of leucocodin R [Staphylococcus aureus]
>gi|1134886|emb|CAA54030.1| glutamine synthetase [Staphylococcus aureus]
>gi|581562|emb|CAA44726.1| fibronectin binding protein B [Staphylococcus aureus]
>gi|550424|emb|CAA57278.1| hlgB-like ORF [Staphylococcus aureus]
>gi|550423|emb|CAA57277.1| hlgC-like ORF [Staphylococcus aureus]
>gi|550422|emb|CAA57276.1| hlgA-like ORF [Staphylococcus aureus]
>gi|468509|emb|CAA54029.1| glutamine synthetase repressor [Staphylococcus aureus]
>gi|468508|emb|CAA54028.1| ORF1 [Staphylococcus aureus]
>gi|311976|emb|CAA50893.1| fibrinogen-binding protein [Staphylococcus aureus]
>gi|311974|emb|CAA50892.1| fibrinogen-binding protein [Staphylococcus aureus]
>gi|296396|emb|CAA50571.1| DNA gyrase [Staphylococcus aureus]
>gi|296395|emb|CAA50570.1| DNA gyrase [Staphylococcus aureus]
>gi|296394|emb|CAA50569.1| RecF [Staphylococcus aureus]
>gi|48713|emb|CAA36830.1| orf145 [Staphylococcus aureus]
>gi|46606|emb|CAA32936.1| lacD polypeptide (AA 1-326) [Staphylococcus aureus]
>gi|46605|emb|CAA32935.1| lacC polypeptide (AA 1-310) [Staphylococcus aureus]
>gi|46589|emb|CAA31770.1| ORF 2 (68 AA) (2187 is 2nd base in codon) [Staphylococcus aureus]
>gi|46588|emb|CAA31769.1| beta-hemolysin (AA 1 - 330) [Staphylococcus aureus]
>gi|46587|emb|CAA31768.1| ORF 1 (AA 1 - 121) (1 is 2nd base in codon) [Staphylococcus aureus]
>gi|46582|emb|CAA35680.1| ORF 419 protein [Staphylococcus aureus]
>gi|46581|emb|CAA35679.1| FemA protein [Staphylococcus aureus]
>gi|46580|emb|CAA35678.1| trpA protein (AA at 1) [Staphylococcus aureus]
>gi|46576|emb|CAA26883.1| Methylase (AA 1-11) (172 is 2nd base in codon) [Staphylococcus aureus]
>gi|809753|emb|CAA26103.1| pot. reading frame C (aa 51-230) (1 is 3rd base in codon) [Staphylococcus aureus]
>gi|736294|emb|CAA68826.1| transposase [Staphylococcus aureus]
>gi|671632|emb|CAA78911.1| unknown [Staphylococcus aureus]
>gi|581558|emb|CAA53189.1| isoleucyl tRNA synthetase [Staphylococcus aureus]
>gi|438228|emb|CAA53191.1| ORF C [Staphylococcus aureus]
>gi|438227|emb|CAA53190.1| ORF B [Staphylococcus aureus]
>gi|49313|emb|CAA78910.1| dihydrofolate reductase [Staphylococcus aureus]
>gi|49018|emb|CAA44472.1| ethidium bromide resistance protein [Staphylococcus aureus]
>gi|49017|emb|CAA44471.1| ethidium bromide resistance protein [Staphylococcus aureus]
>gi|46573|emb|CAA38227.1| ermC [Staphylococcus aureus]
>gi|46571|emb|CAA35972.1| staphylococcal enterotoxin C3 [Staphylococcus aureus]
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>gi|46567|emb|CAA29260.1| enterotoxin C1 precursor (AA -27 to 239) [Staphylococcus aureus]
>gi|46561|emb|CAA33598.1| ethidium bromide resistance protein (AA 1-107) [Staphylococcus aureus]
>gi|46554|emb|CAA68825.1| ORF 140 [Staphylococcus aureus]
>gi|46553|emb|CAA68824.1| dihydrofolate reductase type S1 [Staphylococcus aureus]
>gi|46552|emb|CAA68823.1| thymidylate synthase [Staphylococcus aureus]
>gi|46550|emb|CAA26107.1| pot. reading-frame C (aa 1-90) (4555 is 2nd base in codon) [Staphylococcus aureus]
>gi|46549|emb|CAA26106.1| pot. reading-frame A (aa 1-315) [Staphylococcus aureus]
>gi|46548|emb|CAA26105.1| reading frame D (aa 1-215) chloramphenicol resistance (CAT) [Staphylococcus aureus]
>gi|46547|emb|CAA26104.1| pot. reading-frame B (aa 1-311) pot. replication protein [Staphylococcus aureus]
>gi|4379429|emb|CAA24584.1| reading frame C (replication) [Staphylococcus aureus]
>gi|1333816|emb|CAA24587.1| reading frame D [Staphylococcus aureus]
>gi|1333815|emb|CAA24585.1| reading frame A [Staphylococcus aureus]
>gi|1333813|emb|CAA34365.1| binR product (no atg) [Staphylococcus aureus]
>gi|806585|emb|CAA89212.1| superoxide dismutase [Staphylococcus aureus]
>gi|581555|emb|CAA26630.1| unidentified reading frame put. function in cat regulation [Staphylococcus aureus]
>gi|398182|emb|CAA34366.1| bin3 product [Staphylococcus aureus]
>gi|397526|emb|CAA79304.1| clumping factor [Staphylococcus aureus]
>gi|46540|emb|CAA35664.1| coagulase precursor [Staphylococcus aureus]
>gi|46537|emb|CAA26631.1| chloramphenicol acetyltransferase [Staphylococcus aureus]
>gi|46534|emb|CAA24586.1| CAT (chloramphenicol resistance) [Staphylococcus aureus]
>gi|809610|emb|CAA01358.1| sau3AI M [Staphylococcus aureus]
>gi|580669|emb|CAA01357.1| sau3AI R [Staphylococcus aureus]
>gi|512508|emb|CAA01068.1| fibronectin binding protein [Staphylococcus aureus]
>gi|512504|emb|CAA01067.1| fibronectin binding protein [Staphylococcus aureus]
>gi|512502|emb|CAA01066.1| fibronectin binding protein [Staphylococcus aureus]
>gi|512500|emb|CAA01065.1| fibronectin binding protein [Staphylococcus aureus]
>gi|512498|emb|CAA01064.1| fibronectin binding protein [Staphylococcus aureus]
>gi|512496|emb|CAA01063.1| fibronectin binding protein [Staphylococcus aureus]
>gi|512493|emb|CAA01062.1| fibronectin binding protein [Staphylococcus aureus]
>gi|512491|emb|CAA01061.1| fibronectin binding protein [Staphylococcus aureus]
>gi|512489|emb|CAA01060.1| fibronectin binding protein [Staphylococcus aureus]
>gi|512487|emb|CAA01059.1| fibronectin binding protein [Staphylococcus aureus]
>gi|412259|emb|CAA00843.1| Arp 4 [Staphylococcus aureus]
>gi|412214|emb|CAA00364.1| structural A protein [Staphylococcus aureus]
>gi|412211|emb|CAA00363.1| structural A protein [Staphylococcus aureus]
>gi|765073|gb|AAA99982.1| autolysin
>gi|765072|gb|AAA99981.1| ORF3
>gi|765071|gb|AAA99980.1| ORF2
>gi|765070|gb|AAA99979.1| ORF1
>gi|790573|gb|AAA99709.1| pyrrolidone carboxyl peptidase
>gi|46602|emb|CAA37814.1| putative transposase (AA 1 - 224) [Staphylococcus aureus]
>gi|153077|gb|AAA98349.1| vgh gene product
>gi|581278|emb|CAA26967.1| ORF [Staphylococcus aureus]
>gi|581277|emb|CAA26960.1| tnpA protein [Staphylococcus aureus]
>gi|43733|emb|CAA26966.1| peptide 1 [Staphylococcus aureus]
>gi|43732|emb|CAA26965.1| peptide L [Staphylococcus aureus]
>gi|43731|emb|CAA26964.1| S-adenosyl-methionine dependent methylase [Staphylococcus aureus]
>gi|43730|emb|CAA26963.1| adenyltransferase AAD9 (spc) [Staphylococcus aureus]
>gi|43729|emb|CAA26962.1| pot. tnpC protein [Staphylococcus aureus]
>gi|43728|emb|CAA26961.1| pot. tnpB protein [Staphylococcus aureus]
>gi|1255262|gb|AAA96060.1| phosphoenolpyruvate carboxykinase
>gi|1255260|gb|AAA96059.1| o-succinylbenzoic acid (OSB) synthetase
>gi|1255259|gb|AAA96058.1| o-succinylbenzoic acid (OSB) CoA ligase
>gi|46698|emb|CAA26428.1| put. AAD(9) determinant (aa 1-260) [Staphylococcus aureus]
>gi|46697|emb|CAA26427.1| 3' end of tnpC [Staphylococcus aureus]
>gi|46591|emb|CAA43885.1| Sphingomyelinase [Staphylococcus aureus]
>gi|1196899|gb|AAA88547.1| unknown protein
>gi|153000|gb|AAA88550.1| enterotoxin B
>gi|152949|gb|AAA88549.1| transposase
>gi|152948|gb|AAA88548.1| aminoglycoside resistance protein
>gi|152947|gb|AAA88546.1| transposase
>gi|1181627|gb|AAA86871.1| VAT B
>gi|1016770|gb|AAA86131.1| prolipoprotein diacylglycerol transferase
>gi|705406|gb|AAA82984.1| hyaluronate lyase
>gi|1020317|gb|AAA79506.1| S-adenosylmethionine synthetase
>gi|458420|gb|AAA79365.1| proline permease homolog
>gi|1015409|gb|AAA79055.1| Pre protein

>gi|1015408|gb|AAA79054.1| chloramphenicol acetyltransferase
 >gi|1015407|gb|AAA79053.1| cat leader peptide
 >gi|1015406|gb|AAA79052.1| replication initiation protein
 >gi|915308|gb|AAA74889.1| fibrinogen binding protein
 >gi|409241|gb|AAA74375.1| penicillin-binding protein 2
 >gi|153086|gb|AAA73952.1| DNA gyrase A subunit
 >gi|153085|gb|AAA73951.1| DNA gyrase B subunit
 >gi|153084|gb|AAA73950.1| homologue; putative
 >gi|153062|gb|AAA72091.1| helicase
 >gi|153061|gb|AAA72090.1| [pcrA] gene products
 >gi|152957|gb|AAA71898.1| 5-enolpyruvylshikimate-3-phosphate synthase
 >gi|152956|gb|AAA71897.1| 3-phosphoshikimate-1-carboxyvinyltransferase
 >gi|152955|gb|AAA71896.1| 3-dehydroquinate synthase
 >gi|845687|gb|AAA67855.1| lacA repressor, putative
 >gi|845686|gb|AAA67853.1| ORF-27
 >gi|153035|gb|AAA67854.1| lacR repressor
 >gi|567036|gb|AAA64644.1| CapE
 >gi|506709|gb|AAA64652.1| CapM
 >gi|506708|gb|AAA64651.1| CapL
 >gi|506707|gb|AAA64650.1| CapK
 >gi|506706|gb|AAA64649.1| CapJ
 >gi|506705|gb|AAA64648.1| CapI
 >gi|506704|gb|AAA64647.1| CapH
 >gi|506703|gb|AAA64646.1| CapG
 >gi|506702|gb|AAA64645.1| CapF
 >gi|506700|gb|AAA64643.1| CapD
 >gi|506699|gb|AAA64642.1| CapC
 >gi|506698|gb|AAA64641.1| CapB
 >gi|506697|gb|AAA64640.1| CapA
 >gi|684950|gb|AAA62477.1| staphylococcal accessory regulator A
 >gi|567884|gb|AAA53114.1| lysyl-tRNA synthetase
 >gi|561880|gb|AAA53116.1| gyrase-like protein alpha subunit
 >gi|561879|gb|AAA53115.1| gyrase-like protein beta subunit
 >gi|463285|gb|AAA50463.1| putative
 >gi|551992|gb|AAA26680.1| 25 kD protein (putative); putative
 >gi|551991|gb|AAA26674.1| enterotoxin B
 >gi|495089|gb|AAA26675.1| recombinase
 >gi|398085|gb|AAA26683.1| acetyltransferase
 >gi|153125|gb|AAA26684.1| ATP-binding protein
 >gi|153123|gb|AAA26682.1| toxic shock syndrome toxin-1 precursor
 >gi|153121|gb|AAA26681.1| staphylococcal enterotoxin A precursor
 >gi|153115|gb|AAA26678.1| tetM
 >gi|153106|gb|AAA26677.1| protein A (ttg start codon)
 >gi|153104|gb|AAA26676.1| protein A (ttg start codon)
 >gi|153100|gb|AAA26673.1| Sau3AIM protein
 >gi|153099|gb|AAA26672.1| Sau3AIR protein (ttg start codon)
 >gi|153097|gb|AAA26671.1| bleomycin resistance protein
 >gi|153096|gb|AAA26670.1| neomycin resistance protein
 >gi|153090|gb|AAA26669.1| REP N protein (rep N)
 >gi|153088|gb|AAA26668.1| ethidium resistance protein (ebr)
 >gi|153082|gb|AAA26667.1| recombination and repair protein
 >gi|153080|gb|AAA26666.1| resistance protein
 >gi|153079|gb|AAA26665.1| transposase
 >gi|153067|gb|AAA26662.1| peptidoglycan hydrolase
 >gi|153057|gb|AAA26659.1| nuclease precursor
 >gi|153055|gb|AAA26658.1| norA
 >gi|537341|gb|AAA26647.1| beta-lactamase
 >gi|537340|gb|AAA26646.1| beta-lactamase
 >gi|537339|gb|AAA26645.1| beta-lactamase
 >gi|537338|gb|AAA26644.1| beta-lactamase
 >gi|537337|gb|AAA26643.1| beta-lactamase
 >gi|537336|gb|AAA26642.1| beta-lactamase
 >gi|475839|gb|AAA26654.1| leucocidin S component
 >gi|393266|gb|AAA26634.1| glycerol ester hydrolase
 >gi|295156|gb|AAA26639.1| gamma-hemolysin component B
 >gi|295155|gb|AAA26638.1| gamma-hemolysin component C
 >gi|295154|gb|AAA26637.1| gamma-hemolysin component A
 >gi|295152|gb|AAA26632.1| fibronectin-binding protein precursor
 >gi|153045|gb|AAA26653.1| prolipoprotein signal peptidase
 >gi|153041|gb|AAA26651.1| lincosaminide nucleotidyltransferase
 >gi|153039|gb|AAA26650.1| phospho-beta-galactosidase (lacG)

TABLE 7 : MAP AND SEQUENCE POSITION OF THE 73 ORFs PREDICTED TO BE ENCODED BY PHAGE 44AHJD THAT ARE GREATER THAN 33 AMINO ACIDS

Phage 44AHJD ORFs list

nb	Name	Frame	Position	Size (a.a.)	Key words
1	44AHJDORF001	-1	10342..12627	761	DNA polymerase;
2	44AHJDORF002	3	3789..5732	647	Techoic acid; Staph;
3	44AHJDORF003	2	6626..8389	587	Tail;
4	44AHJDORF004	1	8764..10227	487	Serine protease motif;
5	44AHJDORF005	-1	12643..13890	415	
6	44AHJDORF006	2	803..2029	408	
7	44AHJDORF007	1	2044..3027	327	Upper collar;
8	44AHJDORF008	2	3020..3775	251	Lower collar;
9	44AHJDORF009	2	5744..6496	250	Amidase; Staph;
10	44AHJDORF010	-2	13938..14420	160	
11	44AHJDORF012	3	8391..8813	140	Holin;
12	44AHJDORF013	-2	14586..14996	136	
13	44AHJDORF113	1	199..600	133	
14	44AHJDORF011	-2	15225..15593	122	
15	44AHJDORF114	-2	15870..16172	100	
16	44AHJDORF014	3	6243..6521	92	
17	44AHJDORF015	1	15403..15645	80	
18	44AHJDORF016	-1	15616..15852	78	
19	44AHJDORF017	-2	10536..10757	73	
20	44AHJDORF018	-1	886..1098	70	
21	44AHJDORF019	-2	9630..9836	68	
22	44AHJDORF121	-1	16165..16362	65	
23	44AHJDORF020	2	13865..14053	62	
24	44AHJDORF123	2	614..796	60	
25	44AHJDORF021	-2	5634..5816	60	
26	44AHJDORF023	-2	6315..6494	59	
27	44AHJDORF024	1	14275..14451	58	
28	44AHJDORF025	-3	14999..15175	58	
29	44AHJDORF026	-3	14426..14593	55	
30	44AHJDORF027	1	12916..13080	54	
31	44AHJDORF029	-1	15019..15183	54	
32	44AHJDORF028	-3	9071..9235	54	
33	44AHJDORF030	3	14487..14648	53	
34	44AHJDORF031	2	11039..11191	50	
35	44AHJDORF135	3	693..842	49	
36	44AHJDORF033	-1	3646..3795	49	
37	44AHJDORF032	-2	9306..9455	49	
38	44AHJDORF034	-3	14000..14146	48	
39	44AHJDORF035	-3	13811..13957	48	
40	44AHJDORF036	-3	10019..10165	48	
41	44AHJDORF022	-3	8468..8611	47	
42	44AHJDORF037	1	14788..14931	47	
43	44AHJDORF038	-2	3528..3671	47	
44	44AHJDORF039	3	1743..1883	46	
45	44AHJDORF040	2	9740..9877	45	
46	44AHJDORF041	2	15836..15973	45	
47	44AHJDORF042	-1	5014..5151	45	
48	44AHJDORF043	-1	4402..4539	45	
49	44AHJDORF044	-2	12783..12917	44	
50	44AHJDORF149	-2	639..770	43	
51	44AHJDORF046	1	4891..5019	42	
52	44AHJDORF047	1	11911..12039	42	
53	44AHJDORF045	2	10655..10783	42	
54	44AHJDORF048	-3	15212..15340	42	
55	44AHJDORF049	3	5784..5909	41	
56	44AHJDORF050	3	13158..13283	41	
57	44AHJDORF051	-2	10944..11066	40	
58	44AHJDORF052	-3	14216..14338	40	

TABLE 8: NUCLEOTIDE AND PREDICTED AMINO ACID SEQUENCE OF ALL 73 ORFs IDENTIFIED IN PHAGE 44 AHJD

44AHJDORF001

12627 atgggattactagaatgcatgcaatatcataaacatgaacgtcgaatgattttatactgggatatagaacacattagcgtacaat
1 M G L L E C M Q Y H K H E R R M I L Y W D I E T L A Y N
12543 aaagttaacggcagcaaaaaaaccaacaaatataaaaacgttacttattctgtagcaattggttgggttaatgggtatgaatt
29 K V N G R K K P T K Y K N V T Y S V A I G W F N G Y E I
12459 gatgttgaagtattttccaggttttcgaatctttttatgcagcatttttatacgtatgtgaaaagacgtgatacaatcacaaatca
57 D V E V F P S F E S F Y D A F Y T Y V K R R D T I T K S
12375 aaaacagatattatcatgatgtgcataaactgtaataatcagcaaatcattttttacttaaacacaccatgcggttattttgat
85 K T D I I M I A H N C N K Y D N H F L L K A D T M R Y F D
12291 aatattacacgcgaaaaatatatattttaaactctgcagaagaaaatgaacacacattaaaaatgaaaggagctactatttttagcc
113 N I T R E N I Y L K S A E E N E H T L K M K E A T I L A A
12207 aaaaactcaaaatgtaatttttagaaaaacgtgtaaaactcttcaatcaatttagatttaacaatgtttttaaatgtaattt
141 K N Q N V I L E K R V K S S I N L D L T M F L N G F K F
12123 aatattattgataacttttatgaaaaccaatacatcaattgcaacattaggtgaagaaattacttgatgggtggttatttaacagaa
169 N I I D N F M K T N T S I A T L G K K L L D G G Y L T E
12039 tcacacattaaaacagatttttaattatacgtatttttgataaagcaaatgatatgaatgatagtgcagcctatgactatgctgtg
197 S Q L K T D F N Y T I F D K D N D M N D S E A Y D Y A V
11955 aaatggttttgcaaaactcacacctgaacaacttacatacattcataatgacgtgattatattaggtatgtgccatattcattat
225 K C F A K L T P E Q L T Y I H N D V I I L G M C H I H Y
11871 agtgataattttccaaatttgactatacaaaatttaacatttttcatgtaattatggaactcttacttgaataatgaaatgaca
253 S D I F P N F D Y N K L T F S L N I M E S Y L N N E M T
11787 cgttttcagttactcaaccaatatcaagatatataaaatattcttatacacattatcatttccatgatatgaatttttatgactat
281 R F Q L L N Q Y Q D I K I S Y T H Y H F H D M N F Y D D Y
11703 attaaactcattctatcggtgggttttaaatatgtataacaccaataacatacaaaactaaattgtgagcctgtgttttctatt
309 I K S F Y R G G L N M Y N T K Y I N K L I D E P C F S I
11619 gacatcaattcgagttatccttatgtgatgtatcatgaaaaaattccaacatggtttatacttttcaaacactattcagaacca
337 D I N S S Y P Y V M Y H E K I P T W L Y F Y E H Y S E P
11535 acgttaatccctacttttttagatgatgacaattttttcattataaagattgataaagattgatttaaacgdtatttatta
365 T L I P T T F L D D D N Y F S L Y K I D K D V F N D D L L
11451 attaaaaattaaatcacgtgtattacgtcaaatgattgtaaaaactataaataatgataatgattacgttaatatcaatacaaat
393 I K I K S R V L R Q M I V K Y Y N N D N D Y V N I N T N
11367 acattaaagaatgattcaagacattacgggtattgtgcattgatacgtgttaattcgtttggttatatatgaatgtgaatac
421 T L R M I Q D I T G I D C M H I R V N S F V I Y E C E Y
11283 tttcatgcacgtgatattatttttcaaaactatttttataaaacacaaggtaagttaaaaaacaaaatcaatatgacatcacct
449 F H A R D I I F Q N Y F I K T Q G K L K N K I N M T S P
11199 tacgactatcacattactgatgatatacaacgaaccccatcactcaaatgaggagggttattgttatctaaagtcggttttaaatgga
477 Y D Y H I T D D I N E H P Y S N E E V M L S K V V L N G
11115 ttatatggcatacctgcattacgtttacatttttaacttattccggttagatgataacaatgaactatacaatatcattaacggt
505 L Y G I P A L R S H F N L F R L D D N N E L Y N I I N G
11031 tacaaaaacactgaacgtaatatattattctctacattttgtcattacgtttcattgtatyaacttattgggttcctttccaatc
533 Y K N T E R N I L F S T F V T S R S L Y A N L L V P F Q Y
10947 ttaacggaagtgaaattgacgacaattttattttatgcgatactgatagtttgatatgaaatccggttggttaaaccccttattg
561 L T E S E I D D N F I Y C D T D S L Y M K S V A V V K P L L
10863 aaccccagtttattcgaccgatagccttaggtgaaatgggatattgaaaacgaacagatagataagatgtttgtactgnaatcat
589 N P S L F D P I A L G K W D I E N E Q I D K M F V L N H
10779 aagaaatattgcataatgaagtgaatggaaagattaaaattgcttctgctggtataccgaaaaacgcctttgatacaagcgtcgat
617 K K Y A A Y E V N G K I K I A S A G I P K N A F D T S V D
10695 tttgaaacctttgtacgtgaaacaatttttgcaggtggccattattgaaaacataaaaagtattctaatatgagcaaggtgacaata
645 F E T F V R E Q F F D G A I I E N N K S I Y N E Q G T I
10611 tcgatatatccgtctaaaactgaaattgtatgtggtaatgtatatgatgaatattttactgatgaacttaatatgaaacgtgaa
673 S I Y P S K T E I V C G N V Y D D E Y F T D E L N M K R E
10527 tttatattaaaagacgctagagaaaatttcgacattagtcaatttgatgatattctttatdgaagtgacatcggtttcattt
701 F I L K D A R E N F D H S Q F D D I L Y I E S D I G S F
10443 tcacttaacgacttattttccagttgaacggttcagtacataacaaatctgatttgcatatattaaaacgtgaacatgatgaata
729 S L N D L F P V E R S V H N K S D L H I L K R E H D E I
10359 aaaaaaggcaactgttaa 10342
757 K K G N C *

44AHJDORF002

3789 atggc atataaatgaaaacgatttttaaatatttttgatgacatttcgtccatttttagacgaaatttataaaaacgagagaacgttat
1 M A Y N E N D F K Y F D D I R P F L D E I Y K T T R E R Y
3873 acacggttttacgatgatagacgagattatataactaattcaaaatcatattatgattatatttcaagattatcaaaactaat
29 T P F Y D D R A D Y N T N S K S Y Y D Y I S R L S K L I
3957 gaagtattagcacgtcgtattttgggactatgacaatgaattaaaaaaacgtttcaaaaattgggacgacttaatgaagcattt
57 E V L A R R I W D Y D N E L K K R F K N W D D L M K A F
4041 ccagagcaagcgaaagactattttagaggttggttaaacgacggtacgattgacagttatattcatgacgagtttaaaaaatat
85 P E Q A K D L F R G W L N D G T I D S I I H D E F K K Y
4125 agcgcaggattaacatcggcgttctttttaaagttactgaaatgaacaaatgaatgactttaaatcagaagtttaagaac

113 S A G L T S A F A L F K V T E M K Q M N D F K S E V K D
4209 ttaattaaagatattgaccggttcggttaattgggttgaattaaatgagcttgaaccaaagtttgatgggctttgggtgatt
141 L I K D I D R F V N G F E L N E L E P K F V M G F G G I

4293 cgcaacgcagtttaaccaatctattaatattgataaagaacaaatcacatgtactctacacaatccgattctcaaaaacccgtgaa
169 R N A V N Q S I N I D K E T N H M Y S T Q S D S Q K P E
4377 gggttttggataaaataaacacctagtggtgacttaattcaagcatgcgtattgtacaggggtggtcatggtacaacaatc
197 G F W I N K L T P S G D L I S S M R I V Q G G H G T T I
4461 ggattagaacgtcaatccaatggtgaaatgaaaaatctggttacatcacgatgggtgtgcaaaactggtacaagtgcgcatataaa
225 G L E R Q S N G E M K I W L H H D G V A K L L Q V A Y K
4545 gataaattatgtattagatttagaagaggctaaagggtttaaagattatacaccacagtcacttttaaacacacacacatttaca
253 D N Y V L D L E E A K G L T D Y T P Q S L L N K H T F T
4629 ccgttaattgatgaagcaaatgacaaactcattttaagattcggtgacggaacaatacaggttcggttcaagagcagacgtaaaa
281 P L I D E A N D K L I L R F G D G T I Q V R S R A D V K
4713 aatcacattgataatgataaaaagaatgacaattgataatcagaaaaacaatgataatcggtggatgcaaggcattgctggt
309 N H I D N V E K E M T I D N S E N N D N R W M Q G I A V
4797 gatggatgatgtttatactgggttaagtggttaacagttcagtttaattcacatggtcaaatcggttaaatattcattacaacaggt
337 D G D D L Y W L S G N S S V N S H V Q I G K Y S L T T G
4881 caaagattgtattccatttaagttatcatatcaagacggttatttaatttccacgtgataacttttaagagcctgaggggt
365 Q K I Y D Y P F K L S Y Q D G I N F P R D N F K E P E G
4965 atttgcatttatcaaatccaaaaacaaaacgtaaatcggttattacttgcattgacaaaacggcggtggtggaaaacggttccat
393 I C I Y T T N P K T K R K S L L L A M T N G G G G K R F H
5049 aatttatattggttttccaaacttggtgagttgaacagcttttgagcattacgcgcaagaggttcacaaaactataaaattaca
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5301 cctacaacacaaacattaggtacggttcaagaattaacagctttctcaacaggtcgtaaaatggttaaaatggtgcgtggtatg
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5553 gacgcgccagaaaattaaaaagtggtgcatggttacgtgtgtcaagtggttaacgcagtcggtgaagtagacaaaactta
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5637 gaggtcaatatatcggaatataaagaattcttcagtaattgtaattgcggaacaaaacatcgtaaatatggttgggttagcaaaa
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645 H Q K *

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6962 acacaagggaatttagagcaactctcaaacgtcaatattgaacgtcaacatttatcaaaacgcacgtataactatatgtta
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393 G I L G Q S Q Q A N R Q K N A E S Q L I T N R I D N V L

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7886 aatggtagcgaccgaaatcacgcttttatgacgctgtgagtgtagcaagtaatttaagtcacactgctttatttggtaagttt
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12714 aaagaaaaatatacgaagataactatatagagaatacgaagaaatgatctaatgaacaatatggcctataa 12643
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197 Q P N G Y T P Y N E V C L S D G Y V W I G Y N W Q G T R
6416 tattatttaccagtgcccaatggaatggaaaaacaggttaatagttacagtggttggtatttccttggggggtgttctcataa 6496
225 Y Y L P V R Q W N G K T G N S Y S V G I P W G V F S *

44AHJDORF010

14420 ttggttagacatacgtctgaaatggatagatggaaaaaagaaagagaagctagaaaagagcaagaaaaagatttttttaaat
1 L V R H T S E M D R W K K E R E A R K E Q E K D L F L N
14336 gattttagtaattgttaatttttaatttgatgataaagatttacaagaggcgatcattgacacatggaaacattttgcacatcg
29 D F S N V N F K F D D K D L Q E A Y I D T W K H F A H L
14252 ccctattttcctaagaaagaaacgatatcatatgtaaatgctgtatcatttggttaagaggttcaagacataaaaaattaaattat
57 P Y F P K E R N V S Y V N A V S L V R G S R H K K L N Y
14168 attcttgaaatataaccgtaattgatgtattcttaataaaaaacgctaaaaagcataaatacgttttataattttacaagct
85 I L E I Y N R N D D S N N K N A K K H K Y A L Y N L Q A
14084 aaaaataataattcttcaatgtataaatatattaaagaatcgatactttatataaagaatttggttaaatcagatagaccagtg
113 K N N N S S M Y K Y I K E I D T L Y K E I G K S D R P V
14000 acaaatattgatgatgaatgtgaggtataactttttatattatgcaacatttgacgaataa 13938
141 T N I D D E D V R Y N F L Y Y A T F D E *

44AHJDORF011

15593 atgacaaaacgtaaaagatattttatcaagacacacaaacacattagcgagatttgaatttgaggaaaaaagaaagagaatttatc
1 M T N V K D I L S R H Q N T L A R F E F E E K E R E F I
15509 aaactatcagaatttagtagaaaaatacgggtatgaaaaaagagtatatcggttagagcattattcacaacaaagaatcaaaattc
29 K L S E L V E K Y G M K K E Y I V R A L F T N K E S K F
15425 ggtgaacaagggttatcgctcactgatgactataacgtaaacctaccgaaccacttaacagaattaattaaagaatgagagca
57 G E Q G V I V T D D Y N V N L P N H L T E L I K E M R A
15341 gatgaggacggtgttgacattatcaatgctggagaagttcaattcacaatttatgaatgaaaacaaaaaagggtcaaaaagggt
85 D E D V V D I I N A G E V Q F T I Y E Y E N K K G Q K G
15257 tactcaatcaatttgggtcaagtatcatttaa 15225
113 Y S I N F G Q V S F *

44AHJDORF012

8391 atgaacgaagtaaaattcagatttacagactcagaagcgtttcacatgtttatatacgtctgggattttaaaattactctacttt
1 M N E V K F R F T D S E A F H M F I Y A G D L K L L Y F
8475 ttatttgtattaatgttcgttgatattattacaggtatttcaaaagcaattaaaaataaacttatgggtcaaaaaaatcaatg
29 L F V L M F V D I I T G I S K A I K N N N L W S K K S M
8559 agaggattttctaaaaaattattgatattctgtattatcatttttagcaaacatcattgaccagattttacaattaaaagggtggt
SD-138950.1

57 R G F S K K L L I F C I I I L A N I I D Q I L Q L K G G
 8643 ctactcatgattacaatatattttattatttgcaaatgagggactttctattgtagaaaattgtgcagaaatggacgtattagta
 85 L L M I T I F Y Y I A N E G L S I V E N C A E M D V L V
 8727 ccagaacaaattaaagataaattaagagtcattaaaaatgatactgaaaagagtgataacaatgaacgatcaagagaagataga
 113 P E Q I K D K L R V I K N D T E K S D N N E R S R E D R
 8811 taa 8813
 141 *

44AHJDORF013

14996 atgaaaattaaaactacttttagattaaataattttaattttattaccttttaacaaatagagattattataatgataaatttgaa
 1 M K I K T T F R L N N L I Y Y L L T N R D Y Y N D K F E
 14912 aaatttacttcatctaataaaaaatgtatagtaaaaaataaatatgggtgatgtgtatattgagtttgacaacaatatgatgat
 29 K F T S S N K K C I V K I N M G D V Y I E F D K Q Y D D
 14828 ttgaaattgaaaaagagttttagcttagatctgcacattgatattaaaaaacatgtttttaatacttctgtattttattat
 57 F E I E K E L F T L D I D I D I K K H V F N I L V F Y Y
 14744 agaaattatttaagtaaatgaattaataagagaaattttattaaacgttacaattgacgacgtattatcaaattttgataaacct
 85 R N Y L S N E L I R E I L L N V T I D D V L S N F D K P
 14660 cttgaaagcgaattaatgattattttatcaaaacaaagtcataacgataatgggaaagtgttgaccatgaataa 14586
 113 L E S E L M I I Y Q N K V I Y D N G K V I D H E *

44AHJDORF113

199 atgacagaatttgatgaaatcgtaaaaccagacgacaaaagaagaaacttcagaatcaactgaagaaaatttagaatcaactgaa
 1 M T E F D E I V K P D D K E E T S E S T E E N L E S T E
 283 gaaacttcagaatcaactgaagaatcaactgaagaatcaactgaagaatcaactgaagataaaacagttagaaacaatcgaagaa
 29 E T S E S T E E S T E E S T E E S T E D K T V E T I E E
 367 gaaaatgaaaacaaattagaacctactacaacagatgaagatagttcgaaatttgacctgttgattagaacaacgtattgct
 57 E N E N K L E P T T T D E D S S K F D P V V L E Q R I A
 451 tcattagaacaacaagtgactactttttatcttcacaaatgcaacaaccacaacaagtaacaacaacacaatcagatgtaaca
 85 S L E Q Q V T T F L S S Q M Q Q P Q Q V Q Q T Q S D V T
 535 gaatcaaacaagaagataacgactattcagatgaagaactagttgataagttagatttagattag 600
 113 E S N K E D N D Y S D E E L V D K L D L D *

44AHJDORF114

16172 atgggttaattgtgataatgcaccagaagaaaaaggacaaagcctatactgaaatgttgcaactattcaataaactgattcaatgg
 1 M V N V D N A P E E K G Q A Y T E M L Q L F N K L I Q W
 16088 aatccagcttatacatatttgacaatgcaatttaacttattatcggttgccaacaactattattaaactataatagttctgtgtt
 29 N P A Y T F D N A I N L L S A C Q Q L L L N Y N S S V V
 16004 caattcttaaatgatgaactaaacaacgaaactaaacagaatcaatattgtcttatattgtctggtgatgacccaatagaacaa
 57 Q F L N D E L N N E T K P E S I L S Y I A G D D P I E Q
 15920 tggaatatgcataaaggattttatgaaacgtataacggtttacgttttttag 15870
 85 W N M H K G F Y E T Y N V Y V F *

44AHJDORF014

6243 atgaaaatggtacattttacatgtgggttttttaccatattttgcacgtgtcggtagtccaaaattatcagaacctaatggctatt
 1 M K M V H L H V V F Y Q Y L H V S V V Q N Y Q N L M A I
 6327 gggtccaaccaaacggttataccatataacgaagtttgtttatcagatgggtacgtatggattgggtataactggcaaggca
 29 G S N Q T V I H H I T K F V Y Q M V T Y G L V I T G K A
 6411 cacgttattatttaccagtgcccaatggaatggaaaaacaggttaattacagtggttgattccttggggggtgttctcat
 57 H V I I Y Q C A N G M E K Q V I V T V L V F L G G C S H
 6495 aatgggtatttttagcctttttctttga 6521
 85 N G Y F S L F L *

44AHJDORF015

15403 gtgacgataaacaccttggtcaccgaattttgattccttgggttggaataatgctctaacgatatactcctttttcataccgcat
 1 V T I T P C S P N F D S L F V N N A L T I Y S F F I P Y
 15487 ttttctactaattctgatagtttgataaattctcttcttttctcctcaaatcgaatctcgtaattgtgttttggtgtcttgat
 29 F S T N S D S L I N S L S F S S N S N L A N V F W C L D
 15571 aaaatatcttttacgtttgtcattttatttctcctctattttaattatttgctttctgcaattgcaattgttag 15645
 57 K I S F T F V I L F L L P F K L F A F C N C D L *

44AHJDORF016

15852 atgaaagttgacgacattgttaccttacgtgtcaaggttatatacttcattacttagatgatgataatgaatacattgaggaa
 1 M K V D D I V T L R V K G Y I L H Y L D D D N E Y I E E
 15768 tttttaccacttcacgagatcatcttaacaaaacacaaagcaaaagaaattattaccagacacatgtaaaactattgtccactaca
 29 F L P L H E Y H L T K T Q A K E L L P D T C K L L S T T
 15684 cgcacaacgaaaacaattcaagtttattacaatgatttactacaatcgcaattgcagaaagcaataa 15616
 57 R T T K T I Q V Y Y N D L L Q I A I A E S K *

44AHJDORF017

10757 atggaaagattaaaattgcttctgctggtataccgaaaaacgccttttgatacaagcgtcgattttgaaacctttgtacgtgaac
 1 M E R L K L L L L V Y R K T P L I Q A S I L K P L Y V N
 10673 aattctttgacggtgccattattgaaaacaataaaagtatctataatgagcaaggtacaatatcgatatatccgtctaaaactg
 SD-138950.1

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29 N S L T V P L L K T I K V S I M S K V Q Y R Y I R L K L
10589 aaattgtatgtggtaatgtatatgatgaatattttactgatgaacttaatatga 10536
57 K L Y V V M Y M M N I L L M N L I *

44AHJDORF018

1098 atgttaattgggtactgtgtccataatcacgtattcttcactatattgtccaataaaatcttgctcttttagctaaccaattaaaa
1 M L I G T V S I I T Y S S L Y C P I K S C S L A N Q L K
1014 cgattaccctaataatcgattaataaaagtctcattaatcttagggaataaatattttacaaatgtttcgaacattgta
29 R L P N A I S I N K V S L I L G N K Y L F T N V S N I V
930 ttgaattatcccatttgcgcgaatgtccaagattttgaataa 886
57 F E L S H L S P N V Q D F E *

44AHJDORF019

9836 atgttacctgggtttgtataagtattcttttttgaataaaaggtacaccaattgcttttttatatttttctggtaactgtgcatat
1 M L P G L Y K Y S F L N K G T P I A F L Y F S G N C A Y
9752 gtccagttaccaccaatcacacgaccactttttccatttggcttgactgatttaccactaattgggttatgggtctccgcatca
29 V Q L P P I T R P L F P F G L T D L P L I G L W S P S S
9668 tcagtaggattagaactactactcccactatctactga 9630
57 S V G L E L L L P L S T *

44AHJDORF121

16362 atggaaaatgaaacaaaaaacattgagttgaagcatgtttttcgttttaagaatggaagtttatgtatagcgttatttgataga
1 M E N E T K N I E L K H V F R F K N G S L C I A L F D R
16278 acagaaaatgaaatttcattttatgatgttgacattgatgaaattgaagatttaaatcataattctgttttacgcgtaatttca
29 T E N E I S F Y D V D I D E I E D L N H N S V L R V I S
16194 actttattaggaagtataataatgggttaa 16165
57 T L L G S D N N G *

44AHJDORF020

13865 atgtctaaacgattttgttttaccatgtttttgctccttgtaatagtttatgatgtcgtttacagtgttaaattttattcgtcaa
1 M S K R F C F T M F L L L V I V Y D V V Y S V K F I R Q
13949 atgttgcataatataaaaaagttatacctcacatcttcacatcaatatttgcactgggtctatctgatttaccattttctttat
29 M L H N I K S Y T S H L H H Q Y L S L V Y L I Y Q F L Y
14033 ataaagtatcgatttcttttaa 14053
57 I K Y R F L *

44AHJDORF123

614 atgtatgagggaacaacatgcgttctatgatgggtacatcatatgaagattcaagattaaataaacgaacagaattaaatgaa
1 M Y E G N N M R S M M G T S Y E D S R L N K R T E L N E
698 aacatgtcaattgatacaataaaagtgaagatagttatgggtgtacaaattcattcactttcaaaacaatcatttacaggtgac
29 N M S I D T N K S E D S Y G V Q I H S L S K Q S F T G D
782 gttgaggaggaataa 796
57 V E E E *

44AHJDORF021

5816 atgcaccatcaaagtcaacacctgccccctcatgcttatatatccattcttttgcgttggtgtgatttcattttatatcactc
1 M H H Q S Q H L P P H A Y I S I L L L V V V I S F I S L
5732 ctatttttgatgttttgctacccaaccatattcacgatgttttgcgttcattacattactgaagaattcttttatattccga
29 L F L M F C Y P T I F T M F C F R I N I T E E F F I F R
5648 tatattagcctctaa 5634
57 Y I S L *

44AHJDORF022

8611 atgtttgctaaaatgataatacagaatatcaataatttttagaaaatcctctcattgatttttttgaccataagttattattt
1 M F A A K M I I Q N I N N F L E N P L I D F F D H K L L F
8527 ttaattgcttttgaaatacctgtaataatatcaacgaacattaatacaataaaaaagtag 8468
29 L I A F E I P V I I S T N I N T N K K *

44AHJDORF023

6494 atgagaaccccccaaggaataaccaacactgtaactattacctgtttttccattccattggcgactggtaataataaacgtg
1 M R T P P K E Y Q H C N Y Y L F F H S I G A L V N N N V
6410 tgcttgccagttataaccaatccatacgtacacatctgataacaaacttcgttatatgggtgtataaccggttggttggaacc
29 C L A S Y N Q S I R N H L I N K L R Y M V Y N R L V G T
6326 aatagccattag 6315
57 N S H *

44AHJDORF024

14275 gtgtcaatgtacgcctcttgtaaatctttatcatcaaatttaaaattaacattactaaaatcatttaaaaaataatctttttct
1 V S M Y A S C K S L S S N L K L T L L K S F K N K S F S
14359 tgctcttttctagcttctcttttctttttccatctatccatttcagacgtatgtctaaccaatgttatcaacctccatataaag
29 C S F L A S L S F F H L S I S D V C L T N V I N L H I K
14443 cataaataa 14451
SD-138950.1

CCCTGCGTAA

57 H K *

44AHJDORF025

15175 atggaacgtaaatacaaaaacggtattattatattgcatgagattaaaggacattttccacatcaaatctcaatgtttgaagat
1 M E R K Y K T V L L Y C D E I K G H F P H Q I S M F E D
15091 ttatatgacgctaaagttgtatattcatattatgaatataacctgttcactaaaaatacgcgtatatcatagaatacattaag
29 L Y D A K V V Y S Y Y E Y N L F T K K Y A Y I I E Y I K
15007 gagatataa 14999
57 E I *

44AHJDORF026

14593 atgaataacctattaacatagccattgttttcttttagcatttttaattacacttatcatacttatgacactgcatatacgc
1 M N N L L N I A I V F L L A F L I T L I I L M T L H I R
14509 gtgtcatttggtgttttattcactacattgattatattctatattatcttttaaatggttatttatgcttttatggaggtga 14426
29 V S F G V L F T T L I I F Y I I F L M V I Y A L Y G G *

44AHJDORF027

12916 atgattgtctatatccctaatttttagtacaaaattcatattgttttgtatatggtacaacgataatatttgcataaaagtagt
1 M I V Y I P N F S T K F I L F C I W Y N D N I C H K S S
13000 tacattatacatgactttaatatatttatcatcagttttgatatagaagaatcaccgttttgattgatgtgattttcttaa 13080
29 Y I I H D F N I F I I S F D I E E I T V L I D V I S *

44AHJDORF029

15183 gtgttttaaatggaacgtaaatacaaaaacggtattattatattgcatgagattaaaggacattttccacatcaaatctcaatgt
1 V F K W N V N T K R Y Y Y I A M R L K D I F H I K S Q C
15099 ttgaagatttatatgacgctaaagttgtatattcatattatgaatataacctgttcactaaaaatacgcgtatatcatag 15019
29 L K I Y M T L K L Y I H I M N I T C S L K N T R I S *

44AHJDORF028

9235 atggaatatatgcacgtccaattgtacctgctttcatattttttgcaaaatctgcattaccttttctttgtacgtcttggta
1 M E Y M H V Q L Y L L S Y F L Q N L H Y L F F V R L V V
9151 caaagtggacgatgttacctgcgtcataccaagacggttgctccagctgttttgattgtgataacttttctgtcatga 9071
29 Q S G R C Y L R H T K T V V Q L V L I V I L T F L L *

44AHJDORF030

14487 gtgaataaaacaccaaataacacgcgtatatgcagtgatagataagtgataattaaaaatgctaaaaggaaaacaatg
1 V N K T P N D T R I C S V I S M I S V I K N A K R K T M
14571 gctatgtttaataggttattcatgggtcaatcactttccattatcgatatgactttgttttgataaataatcattaa 14648
29 A M F N R L F M V N H F P I I V Y D F V L I N N H *

44AHJDORF031

11039 atgatattgtatagttcattgttatcatctaaacggaataagttaaaatgtgaacgtaatgcaggtatgccatataatccattt
1 M I L Y S S L L S S K R N K L K C E R N A G M P Y N P F
11123 aaaacgacttttagataacataacctcctcatttgagtatgggtgttcgttgatatcatcagtaagtga 11191
29 K T T L D N I T S S F E Y G C S L I S S V M *

44AHJDORF135

693 atgaaaacatgtcaattgatacaataaaagtgaagatagttatgggtgtacaaattcattcactttcaaaacaatcatttacag
1 M K T C Q L I Q I K V K I V M V Y K F I H F Q N N H L Q
777 gtgacgttgaggaggaataataaattatggcacaacaatctacaaaaaatgaaactgcacttttag 842
29 V T L R R N N K L W H N N L Q K M K L H F *

44AHJDORF033

3795 atgccattatttaaccacctctaccaaatgtgtaaaaaacatttttatcaaattcatttaaaattttctttcttaaatcgta
1 M P L F N H L Y Q I C K K H F L S N S F K I F F L K S Y
3711 gctttatcaatattatcaattaaatactgcttagtgatgtgtaccttttgacattacctttttga 3646
29 A L S I L S I K Y C L V N C V P F A L P F *

44AHJDORF032

9455 atggcttgttttgctaaagcgagtagtgaaactaccactgtcaccactactaccactgtcagacgaatcactaggtgatccacct
1 M A C F A K A S S E L P L S P L L P L S D E S L G D P P
9371 ttaccgtctaatttaccaccccaagctagaatagtattcgcaccgtctaaaaatggattaccatag 9306
29 L P S N L P P Q A R I V F A P S K N G L P *

44AHJDORF034

14146 atgatgattctaataataaaaacgctaaaaagcataaatacgcgtttatataatttacaagctaaaaataataattcttcaatgt
1 M M I L I I K T L K S I N T L Y I I Y K L K I I I L Q C
14062 ataaatatattaaagaaatcgatactttatataaagaaattggtaaatcagatagaccagtga 14000
29 I N I L K K S I L Y I K K L V N Q I D Q *

44AHJDORF035

13957 atgcaacatttgacgaataaatttaacactgtaaacgacatcataaactattacaaggagcaaaaacatggtaaaacaaaatcg
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 13873 tttagacatggtaagagattatcaaaatgctgtcaatcatgtcagaaaaaaatcccagataa 13811
 29 F R H G K R L S K C C Q S C Q K K N P R *

44AHJDORF036

10165 gtgtatacaataccacacgtgatgggtgaacatatgggtgtacattatagtttgcaactaaaaacgaaccatcttcaaaaactg
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 10081 ctacaacaacacctgtgtgaccaataccatattgcagttgcttgaagtatgggtggtttactag 10019
 29 L Q Q H L C D Q Y H M Q L L V S M V V Y *

44AHJDORF037

14788 atgtcgatatctaacgtaaaataactctttttcaatttcaaaatcatcatattgtttgtcaaactcaatatacacatcacccata
 1 M S I S N V N N S F S I S K S S Y C L S N S I Y T S P I
 14872 tttatttttactatacatctttttattagatgaagtaatttttcaatttatcattataa 14931
 29 F I F T I H F L L D E V N F S N L S L *

44AHJDORF038

3671 gtgtaccttttgcattaccttttggattttgattacgttttgcgttttgattactttcgttactcgatttattcacagttttac
 1 V Y L L H Y L F D F D Y V L R F D Y F R Y S I Y S Q F Y
 3587 cgttatcaatcgattattatcagcgaatcgtaacgttgtattatcaacatcaatgtaa 3528
 29 R Y Q S Y Y Y Q R I V T L Y Y Q H Q C *

44AHJDORF039

1743 gtgctgtattttacttatgatgtatctaaacttaaagagtttactggcaacgttgaagaaattaaacaaaatcagatttatatg
 1 V L Y L L M M Y L N L K S L L A T L K K L N Q N Q I Y M
 1827 cgtttattttggatattaattcaattaaataaaacgtttacacaaaaggatgtaa 1883
 29 R L F W I L I Q L N I N V T Q K V C *

44AHJDORF040

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 1 V V T G H M H S Y Q K N I K K Q L V Y L Y S K K N T Y T
 9824 aaccaggtaacatatcttctcaaacgggtaatgcaggacaatgtacagaattaa 9877
 29 N Q V T Y F L K R V M Q D N V Q N *

44AHJDORF041

15836 atgtcgtaactttcattattatatcactccttttctaaaaaacgtaaacgtttatcgtttcataaaatcctttatgcatattcc
 1 M S S T F I I I S L L S K K R K R Y T F H K I L Y A Y S
 15920 attgttctattgggtcatcaccagcaatataagacaatattgattctggtttag 15973
 29 I V L L G H H Q Q Y K T I L I L V *

44AHJDORF042

5151 atgcacgacgcgtcgtcttttggtaatttatagttttgtgaacctcttgcgcgtaatgcttcaaagtgttcataactcaccaagtt
 1 M H D R R L L L I Y S F V N L L R V M L Q S V H T H Q V
 5067 ggaagaaacatatataaattatggaacgttttccaccaccgcggtttgtcatag 5014
 29 G R N H I N Y G N V F H H R R L S *

44AHJDORF043

4539 atgcgacttgtaacagttttgcaacaccatcgatgtgaaccagattttcatttcaccattggattgacgttctaataccgattg
 1 M R L Q L T V L Q H H R D V T R F S F H H W I D V L I R L
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 29 L Y H D H P V Q Y A C L K L S H H *

44AHJDORF044

12917 atgttacctattttacgtgatgatattgtttataaagaaaacatggaacgttattactacaatccaagcaattttacattttgaca
 1 M L P I Y V M I C F I K K T W N V I T T I Q A I Y I L T
 12833 atgcttactctaaaaattacgtgggttgataatgatagatatttatatttag 12783
 29 M L T L K I T W L I M I D I Y I *

44AHJDORF149

770 atgattgttttgaaagtgaatgaatttgtacaccataactatcttcacttttatttgtatcaattgacatgttttcatttaatt
 1 M I V L K V N E F V H H N Y L H F Y L Y Q L T C F H L I
 686 ctgttcggtttatttaattcttgatcttcatatgatgtaccatcatag 639
 29 L F V Y L I L N L H M M Y P S *

44AHJDORF046

4891 atgattatccattttaagttatcatatcaagacggattattaatttcccacgtgataacttttaagagcctgagggtattttgcattt
 1 M I I H L S Y H I K T V L I S H V I T L K S L R V F A F
 4975 atacaaatccaaaacaaaacgtaaatcgttattacttgctatga 5019
 29 I Q I Q K Q N V N R Y Y L L *

$\frac{1}{\sqrt{2}} \begin{pmatrix} 1 & i \\ 1 & -i \end{pmatrix}$	$\frac{1}{\sqrt{2}} \begin{pmatrix} 1 & -i \\ 1 & i \end{pmatrix}$	$\frac{1}{\sqrt{2}} \begin{pmatrix} 1 & 1 \\ i & -i \end{pmatrix}$	$\frac{1}{\sqrt{2}} \begin{pmatrix} 1 & -1 \\ i & i \end{pmatrix}$	$\frac{1}{\sqrt{2}} \begin{pmatrix} 1 & i \\ -1 & -i \end{pmatrix}$	$\frac{1}{\sqrt{2}} \begin{pmatrix} 1 & -i \\ -1 & i \end{pmatrix}$	$\frac{1}{\sqrt{2}} \begin{pmatrix} 1 & 1 \\ -i & i \end{pmatrix}$	$\frac{1}{\sqrt{2}} \begin{pmatrix} 1 & -1 \\ -i & -i \end{pmatrix}$
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SD-138950.1

44AHJDORF058

10767 atgcatatttcttatgattcagtaacacatcttatctctgttcgttttcaatatcccatctacctaaggctatcggtcga
1 M H I S Y D S V Q T S Y L S V R F Q Y P I Y L R L S G R
10851 ataaactggggttcaataagggtttaa 10877
29 I N W G S I R V *

44AHJDORF164

702 atgttttcatttaattctgttcgtttatattaatcttgaatcttcatatgatgtacccatcatagaacgcattgtgtttccctca
1 M F S F N S V R L F N L E S S Y D V P I I E R M L F P S
618 tacatgtttaaatctctctaattctaa 592
29 Y M F K F L L I *

44AHJDORF059

8360 atggattttgtaacattggattacctgaaccgtcattatgccaaaatcttacaccagattctaaaattgcttttaattgttcca
1 M D F V T L D Y L N R H Y A K I L H Q I L K L L L I V P
8276 ttaacatggggtcgatgtcacgtatag 8250
29 L T W G R C H V *

44AHJDORF060

6257 atgtaccattttcatttctataatatgtgccgtattggtttcgtttccattttccaaatgtatttacttttgatgtttctaag
1 M Y H F H F Y N M C R I G F V S I F Q M Y L L L M F L M
6173 ctttgcattactacctgaaaatttag 6147
29 L C Y Y Y L K I *

44AHJDORF061

15551 atgtgttttggtgtcttgataaaatatcttttacgtttgtcattttatttctctcttattttaaattatttgctttctgcaatt
1 M C F G V L I K Y L R L S F Y F S S Y L N Y L L S A I
15635 gcgattttagtaaatcattgtaa 15658
29 A I C S K S L *

44AHJDORF062

4285 gtggtattcgcaacgcagttaaccaatctattaatttgataaagaaacaaatcacatgtactctacacaatccgattctcaaa
1 V V F A T Q L T N L L I L I K K Q I T C T L H N P I L K
4369 aacctgaagggtttttggataa 4389
29 N L K V F G *

44AHJDORF063

9487 atgcgtcttgatttttttaataattcttgcattggttgttttgctaagcgagtagtgaactaccactgtcaccactactac
1 M R L V F F L I I L A W L V L L K R V V N Y H C H H Y Y
9403 cactgtcagacgaatcactag 9383
29 H C Q T N H *

44AHJDORF065

5029 gtggtggaaaaacgtttccataatttatatggtttcttccaacttggtgagtagatgaacactttgaagcattacgcgcaagaggtt
1 V V E N V S I I Y M V S S N L V S M N T L K H Y A Q E V
5113 cacaaaactataaattaa 5130
29 H K T I N *

44AHJDORF064

2609 atgacgagtcattcaatcaacttgtgtccgaaatatataacggtgcaccatttgttaaaatgtcacctatgtttaatgcagatg
1 M T S Q S I N L C P K Y I T V H H L L K C H L C L M Q M
2693 acgatattcattgatttaa 2710
29 T I S L I *

44AHJDORF066

10481 atgatattctttatattgaaagtacatcggttcattttcacttaacgacttatttccagttgaacgttcagtacataacaaat
1 M I F F I L K V T S V H F H L T T Y F Q L N V Q Y I T N
10397 ctgatttgcataatattaa 10380
29 L I C I Y *